GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 12:03:09 ; Search time 2816.55 Seconds
(without alignments)
17469.212 Million cell updates/sec

Title: US-09-135-010A-1
Perfect score: 3181
Sequence: 1 ctgccccctccggccccgcc.....aataaacgtggagaatcaca 3181

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 12

Total number of hits satisfying chosen parameters: 477188

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
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94: gb_ro1:*
95: gb_ro2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 3076 | 96.7 | 3129 | 88 | AF000571 | AF000571 Homo sapi |
| 2 | 2702 | 84.9 | 2821 | 97 | HSU89364 | U89364 Homo sapien |
| 3 | 1637 | 51.5 | 2144 | 88 | AF051426 | AF051426 Homo sapi |
| 4 | 1227 | 38.6 | 104123 | 93 | HSA6345_3 | Continuation (4 of |
| 5 | 1176 | 37.0 | 137932 | 86 | AC005950 | AC005950 Homo sapi |
| c 6 | 1176 | 37.0 | 181483 | 63 | AC013791 | AC013791 Homo sapi |
| 7 | 1074 | 33.8 | 244254 | 93 | HSAC001228 | AC001228 244Kb Con |
| 8 | 548 | 17.2 | 155074 | 85 | AC003693 | AC003693 Human Chr |

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| 9 | 398 | 12.5 | 471 | 85 | AB01514S02 | AB015148 Homo sapi |
| 10 | 386 | 12.1 | 386 | 97 | HSU86146 | U86146 Human volta |
| 11 | 278 | 8.7 | 298 | 85 | AB01514S17 | AB015163 Homo sapi |
| 12 | 206 | 6.5 | 110000 | 93 | HSA6345_0 | AJ006345 Homo sapi |
| 13 | 163 | 5.1 | 304 | 88 | AF003743 | AF003743 Homo sapi |
| 14 | 148 | 4.7 | 160847 | 70 | AC026645 | AC026645 Homo sapi |
| 15 | 145 | 4.6 | 237 | 85 | AB01514S07 | AB015153 Homo sapi |
| c 16 | 145 | 4.6 | 6394 | 93 | HSM802644 | AL353939 Homo sapi |
| 17 | 145 | 4.6 | 110000 | 93 | HSA6345_1 | Continuation (2 of |
| 18 | 145 | 4.6 | 111324 | 85 | AC000377 | AC000377 Human Chr |
| c 19 | 145 | 4.6 | 132960 | 85 | AC002403 | AC002403 Human Chr |
| 20 | 143 | 4.5 | 212 | 85 | AB01514S11 | AB015157 Homo sapi |
| c 21 | 143 | 4.5 | 78064 | 84 | HSAC000376 | AC000376 Homo sapi |
| 22 | 129 | 4.1 | 208 | 85 | AB01514S10 | AB015156 Homo sapi |
| 23 | 128 | 4.0 | 198 | 85 | AB01514S04 | AB015150 Homo sapi |
| 24 | 123 | 3.9 | 178 | 85 | AB01514S12 | AB015158 Homo sapi |
| 25 | 123 | 3.9 | 110000 | 93 | HSA6345_2 | Continuation (3 of |
| c 26 | 123 | 3.9 | 120229 | 97 | U90095 | U90095 Human Chrom |
| c 27 | 123 | 3.9 | 172988 | 66 | AC021424 | AC021424 Homo sapi |
| 28 | 113 | 3.6 | 195 | 85 | AB01514S08 | AB015154 Homo sapi |
| 29 | 101 | 3.2 | 151 | 85 | AB01514S06 | AB015152 Homo sapi |
| 30 | 99 | 3.1 | 86621 | 85 | AC003675 | AC003675 Human Chr |
| 31 | 97 | 3.0 | 191 | 85 | AB01514S09 | AB015155 Homo sapi |
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| 33 | 92 | 2.9 | 168 | 85 | AB01514S01 | AB015147 Homo sapi |
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| 35 | 76 | 2.4 | 140 | 85 | AB01514S13 | AB015159 Homo sapi |
| 36 | 66 | 2.1 | 277 | 85 | AB01514S16 | AB015162 Homo sapi |
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| 39 | 50 | 1.6 | 178 | 85 | AB01514S14 | AB015160 Homo sapi |
| 40 | 49 | 1.5 | 248 | 85 | AB01514S15 | AB015161 Homo sapi |
| 41 | 44 | 1.4 | 881 | 95 | RNU92655 | U92655 Rattus norv |
| 42 | 44 | 1.4 | 3070 | 95 | RNO133685 | AJ133685 Rattus no |
| 43 | 42 | 1.3 | 516 | 7 | AF013961 | AF013961 Felis cat |
| 44 | 41 | 1.3 | 300 | 94 | AF049341 | AF049341 Cavia por |
| 45 | 41 | 1.3 | 2841 | 94 | MMU70068 | U70068 Mus musculu |

ALIGNMENTS

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RESULT   1
AF000571
LOCUS       AF000571     3129 bp    mRNA            PRI       06-OCT-1997
DEFINITION  Homo sapiens kidney and cardiac voltage dependent K+ channel
            (KvLQT1) mRNA, complete cds.
ACCESSION   AF000571
VERSION     AF000571.1  GI:2465530
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3129)
  AUTHORS   Chouabe,C., Neyroud,N., Guicheney,P., Lazdunski,M., Romey,G. and
            Barhanin,J.
  TITLE     Properties of KvLQT1 K+ channel mutations in Romano-Ward and
            Jervell and Lange-Nielsen inherited cardiac arrhythmias
  JOURNAL   EMBO J. 16 (17), 5472-5479 (1997)
  MEDLINE   97459933
REFERENCE   2  (bases 1 to 3129)
  AUTHORS   Barhanin,J., Romey,G. and Lazdunski,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-APR-1997) IPMC, CNRS, route des lucioles,
            Sophia-Antipolis, Valbonne 06560, France
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                     RTHVQGRVYNFLERPTGWKCFVYHFAVFLIVLVCLIFSVLSTIEQYAALATGTLFWME
                     IVLVVFFGTEYVVRLWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVASMVVLCVGSK
                     GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFS
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                     FAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSSTW
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                     RRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPITHISQLRE
                     HHRATIKVIRRMQYFVAKKKFQQARKPYDVRDVIEQYSQGHLNLMVRIKELQRRLDQS
                     IGKPSLFISVSEKSKDRGSNTIGARLNRVEDKVTQLDQRLALITDMLHQLLSLHGGST
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BASE COUNT      579 a   1041 c    952 g    557 t
ORIGIN
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Query Match 96.7%; Score 3076; DB 88; Length 3129;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3126; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     115 ctcccggtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcc 174
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Qy     535 taccacttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccacc 594
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ACCESSION   U89364 U40990 U71077
VERSION     U89364.1  GI:2465514
KEYWORDS    .
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 189 to 2821)
  AUTHORS   Wang,Q., Curran,M.E., Splawski,I., Burn,T.C., Millholland,J.M.,
            VanRaay,R.J., Shen,J., Timothy,K.W., Vincent,G.M., de Jager,T.,
            Schwartz,P.J., Towbin,J.A., Moss,A.J., Atkinson,D.L., Landes,G.M.,
            Connors,T.D. and Keating,M.T.
  TITLE     Positional cloning of a novel potassium channel gene: KVLQT1
            mutations cause cardiac arrhythmias
  JOURNAL   Nature Genet. 12 (1), 17-23 (1996)
  MEDLINE   96122034
REFERENCE   2  (bases 1 to 270)
  AUTHORS   Sanguinetti,M.C., Curran,M.E., Zou,A., Shen,J., Spector,P.S.,
            Atkinson,D.L. and Keating,M.T.
  TITLE     Coassembly of K(V)LQT1 and minK (IsK) proteins to form cardiac
            I(Ks) potassium channel
  JOURNAL   Nature 384 (6604), 80-83 (1996)
  MEDLINE   97055938
REFERENCE   3  (bases 1 to 2821)
  AUTHORS   Splawski,I., Timothy,K.W., Vincent,G.M., Atkinson,D.L. and
            Keating,M.T.
  TITLE     Molecular basis of the long-QT syndrome associated with deafness
  JOURNAL   N. Engl. J. Med. 336 (22), 1562-1567 (1997)
  MEDLINE   97291362
REFERENCE   4  (bases 1 to 2821)
  AUTHORS   Splawski,I., Timothy,K.W., Vincent,G.M., Atkinson,D.L. and
            Keating,M.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-1997) Howard Hughes Medical Institute, University
            of Utah, 10 North 2030 East Street, Salt Lake City, UT 84112, USA
COMMENT     On Oct 7, 1997 this sequence version replaced gi:1147606
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VERSION AF051426.1 GI:2961248
KEYWORDS .
SOURCE human.

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REFERENCE   1  (bases 1 to 2144)
  AUTHORS   Jiang,M., Tseng-Crank,J. and Tseng,G.N.
  TITLE     Suppression of slow delayed rectifier current by a truncated
            isoform of KvLQT1 cloned from normal human heart
  JOURNAL   J. Biol. Chem. 272 (39), 24109-24112 (1997)
  MEDLINE   97450920
REFERENCE   2  (bases 1 to 2144)
  AUTHORS   Jiang,M., Tseng-Crank,J. and Tseng,G.-N.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-1998) Pharmacology, Columbia University, 630 W.
            168th Street, New York, NY 10032, USA
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BASE COUNT      410 a    670 c    652 g    412 t
ORIGIN
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  Query Match           51.5%;  Score 1637;  DB 88;  Length 2144;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1877;  Conservative    0;  Mismatches    0;  Indels    3;  Gaps    1;

Qy    549 cttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcagtatgc 608
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Db    262 CTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGTGCTGTCCACCATCGAGCAGTATGC 321

Qy    609 cgccctggccacggggactctcttctggatggagatcgtgctggtggtgttcttcgggac 668
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Qy    669 ggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcctctgggg 728
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Db    382 GGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCGCAGCAAGTACGTGGGCCTCTGGGG 441

Qy    729 gcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtggcctc 788
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Db    442 GCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCATCGACCTCATCGTGGTCGTGGCCTC 501

Qy    789 catggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggccatcagggg 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 CATGGTGGTCCTCTGCGTGGGCTCCAAGGGGCAGGTGTTTGCCACGTCGGCCATCAGGGG 561

Qy    849 catccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggcacctggag 908
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Db    562 CATCCGCTTCCTGCAGATCCTGAGGATGCTACACGTCGACCGCCAGGGAGGCACCTGGAG 621

Qy    909 gctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctgtacatcgg 968
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Db    622 GCTCCTGGGCTCCGTGGTCTTCATCCACCGCCAGGAGCTGATAACCACCCTGTACATCGG 681

Qy    969 cttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggacgcggtgaa 1028
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Qy   1029 cgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggggggtggtcac 1088
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Db    742 CGAGTCAGGCCGCGTGGAGTTCGGCAGCTACGCAGATGCGCTGTGGTGGGGGGTGGTCAC 801

Qy   1089 agtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaagaccatcgc 1148
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Db    802 AGTCACCACCATCGGCTATGGGGACAAGGTGCCCCAGACGTGGGTCGGGAAGACCATCGC 861

Qy   1149 ctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggattcttggctc 1208
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Qy   1329 ctccacctggaagatctacatccggaaggccccccggagccacactctgctgtcacccag 1388
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Qy   1389 ccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggacaaagacaa 1448
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Qy   1449 tggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgacccccccaga 1508
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Db   1159 TGGGGTGACTCCTGGAGAGAAGATGCTCACAGTCCCCCATATCACGTGCGACCCCCCAGA 1218

Qy   1509 agagcggcggctggaccacttctctgtcgacggctatgacagttctgtaaggaagagccc 1568
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Qy   1569 aacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgccgaggacct 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1629 ggacctggaaggggagactctgctgacacccatcacccacatctcacagctgcgggaaca 1688
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Qy   1689 ccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaagaagaaatt 1748
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Qy   1749 ccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcgcagggcca 1808
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Qy   1809 cctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtccattgggaa 1868
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Db   1699 CACCGACATGCTTCACCAGCTGCTCTCCTTGCACGGTGGCAGCACCCCCGGCAGCGGCGG 1758

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Qy   2109 ccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtgcccag 2168
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Qy   2169 gaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcctgagtgag 2228
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Qy   2229 aggggaggccaagagtggccccacctggccctctctgaaggaggccacctcctaaaaggc 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1939 AGGGGAGGCCAAGAGTGGCCCCACCTGGCCCTCTCTGAAGGAGGCCACCTCCTAAAAGGC 1998

Qy   2289 ccagagagaagagccccactctcagaggccccaataccccatggaccatgctgtctggca 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1999 CCAGAGAGAAGAGCCCCACTCTCAGAGGCCCCAATACCCCATGGACCATGCTGTCTGGCA 2058

Qy   2349 cagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggggccccgtc 2408
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Db   2059 CAGCCTGCACTTGGGGGCTCAGCAAGGCCACCTCTTCCTGGCCGGTGTGGGGGCCCCGTC 2118

Qy   2409 tcaggtctgagttgttaccc 2428
          ||||||||||||||||||||
Db   2119 TCAGGTCTGAGTTGTTACCC 2138


RESULT   4
HSA6345_3
WPCOMMENT
  Sequence split into 4 fragments  LOCUS HSA6345 Accession AJ006345
     Fragment Name      Begin     End
     HSA6345_0              1     110000
     HSA6345_1         100001     210000
     HSA6345_2         200001     310000
     HSA6345_3         300001     404123
Continuation (4 of 4) of HSA6345 from base 300001 (AJ006345 Homo sapiens KVLQT1 gene. 6/


  Query Match            38.6%;  Score 1227;  DB 93;  Length 104123;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2075 tcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaaca 2134
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Db 102792 TCACCCAGCCCTGCGGCAGTGGCGGCTCCGTCGACCCTGAGCTCTTCCTGCCCAGCAACA 102851

Qy   2135 ccctgcccacctacgagcagctgaccgtgcccaggaggggcccccgatgaggggtcctgag 2194
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Qy   2195 gaggggatggggctgggggatgggcctgagtgagaggggaggccaagagtggccccacct 2254
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Qy   2255 ggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcaga 2314
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Qy   2315 ggccccaataccccatggaccatgctgtctggcacagcctgcacttgggggctcagcaag 2374
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Qy   2375 gccacctcttcctggccggtgtgggggccccgtctcaggtctgagttgttaccccaagcg 2434
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Db 103812 GATTTGGATCTGTGTTTTAATGAGTTTCACAGTGTGATTTTGATTATTAATTGTGCAAGC 103871

Qy   3155 ttttcctaataaacgtggagaatcaca 3181
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RESULT   5
AC005950
LOCUS       AC005950   137932 bp    DNA             PRI       07-NOV-1998
DEFINITION  Homo sapiens Chromsome 11p15.5 PAC clone pDJ754h15 containing
            cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence.
ACCESSION   AC005950
VERSION     AC005950.1  GI:3850601
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 137932)
  AUTHORS   Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
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            Buettner,J., Bumeister,R., Card,P., deSailboat,F., Dunn,J.,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
            Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
            Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.
  TITLE     HTGS Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 137932)
  AUTHORS   Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
            Buettner,J., Butler,C., Card,P., deSailboat,F., Dunn,J.,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
            Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
            Schageman,J., Schultz,R.A., Stimson,S., Waller,K. and Ward,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-NOV-1998) Genome Science & Technology Center,
            University of Texas Southwestern Medical Center, 5323 Harry Hines
            Blvd, Dallas, TX 75235-8591, USA
COMMENT     IMPORTANT: This submission contains the entire insert of clone
            pDJ754h15.  pDJ754h15 comes from the RPCI-3 PAC library constructed
            at the Roswell Park Cancer Institute by the Pieter de Jong group.
            This clone has been finished according to strict quality criteria
            and attempts have been made to resolve all base calling problems
            such as compressions and repetitive elements.  The expected
            Phred/Phrap calculated errors/10kb is 0.97.  In addition, attempts
            have been made to assure over 99% of consensus base calls consist
            of either double-stranded coverage or 2 types of labeling chemistry
            on one strand.
            CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome 11p15.5
            Wilms tumor type 2 (WT2) region between ESTs CTSD and IGF2(INSL2).
            This region spanning approximately 2 Mbp is mapped between D11S2701
            and D11S1145.
FEATURES             Location/Qualifiers
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ORIGIN


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  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1226;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1955 aggtgacgcagctggaccagaggctggcactcatcaccgacatgcttcaccagctgctct 2014
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Db  51300 AGGTGACGCAGCTGGACCAGAGGCTGGCACTCATCACCGACATGCTTCACCAGCTGCTCT 51359

Qy   2015 ccttgcacggtggcagcacccccggcagcggcggccccccagagagggcggggcccaca 2074
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Qy   2075 tcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaaca 2134
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Qy   2195 gaggggatggggctgggggatgggcctgagtgagaggggaggccaagagtggccccacct 2254
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Qy   2255 ggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcaga 2314
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Qy   2315 ggccccaataccccatggaccatgctgtctggcacagcctgcacttgggggctcagcaag 2374
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Qy   2435 ccctggccccccacatggtgatgttgacatcactggcatggtggttgggacccagtggcag 2494
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Qy   2555 tgcttggcccaggggggcttcctgaggggagacagagcaacccctggaccccagcctcaaa 2614
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Qy   2795 gagggacagtctcaccatttccccagggcacgtggttgagtgggggggaacgcccacttcc 2854
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LOCUS       AC013791   181483 bp    DNA             HTG       19-JAN-2001
DEFINITION  Homo sapiens clone RP11-19N21, WORKING DRAFT SEQUENCE, 9 unordered
            pieces.
ACCESSION   AC013791
VERSION     AC013791.4  GI:12313824
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 181483)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-19N21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 181483)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
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            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
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            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jan 19, 2001 this sequence version replaced gi:7382100.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L3857
                Center clone name: 19_N_21
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 47% of reads
                Sequencing vector: Plasmid; n/a; 53% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 176802 bases at least Q40
                Consensus quality: 179250 bases at least Q30
                Consensus quality: 180075 bases at least Q20
                Insert size: 173000; agarose-fp
                Insert size: 180683; sum-of-contigs
                Quality coverage: 10.2 in Q20 bases; agarose-fp
                Quality coverage: 9.8 in Q20 b.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 9 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *    35936 36035: gap of      100 bp
            *    36036    37309: contig of 1274 bp in length
            *    37310 37409: gap of      100 bp
            *    37410    38442: contig of 1033 bp in length
            *    38443 38542: gap of      100 bp
            *    38543    40094: contig of 1552 bp in length
            *    40095 40194: gap of      100 bp
            *    40195    41451: contig of 1257 bp in length
            *    41452 41551: gap of      100 bp
            *    41552    42812: contig of 1261 bp in length
            *    42813 42912: gap of      100 bp
            *    42913    63014: contig of 20102 bp in length
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ORIGIN


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Qy    1955 aggtgacgcagctggaccagaggctggcactcatcaccgacatgcttcaccagctgctct 2014
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Qy    2015 ccttgcacggtggcagcacccccggcagcggcggcccccccagagagggcggggcccaca 2074
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Qy    2075 tcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaaca 2134
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Qy    2135 ccctgcccacctacgagcagctgaccgtgcccaggaggggccccgatgaggggtcctgag 2194
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Qy    2255 ggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcaga 2314
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Qy    2375 gccacctcttcctggccggtgtgggggccccgtctcaggtctgagttgttaccccaagcg 2434
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Qy    2435 ccctggcccccacatggtgatgttgacatcactggcatggtggttgggacccagtggcag 2494
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Qy    2495 ggcacagggcctggcccatgtatggccaggaagtagcacaggctgagtgcaggcccaccc 2554
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Qy    2555 tgcttggcccaggggggcttcctgaggggagacagagcaaccccctggaccccagcctcaaa 2614
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Qy    2615 tccaggaccctgccaggcacaggcagggcaggaccagcccacgctgactacagggccacc 2674
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Qy    2675 ggcaataaaagcccaggagcccatttggagggcctgggcctggctccctcactctcagga 2734
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Qy    2735 aatgctgacccatgggcaggagactgtggagactgctcctgagccccccagcttccagcag 2794
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Qy    2795 gagggacagtctcaccatttccccagggcacgtggttgagtgggggggaacgcccacttcc 2854
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Qy    2915 ccactgtgcgtggggctcccgcctccaaccccctcgcccagtcccagcagccagccaaaca 2974
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Qy    3035 ctacacaggacaggggttccttctgggcattacatcgcatagaaatcaataatttgtggt 3094
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Qy    3155 ttttcctaataaaacgtggagaatcaca 3181
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RESULT  7
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LOCUS       HSAC001228 244254 bp    DNA             PRI       14-APR-1997
DEFINITION  244Kb Contig from Human Chromsome 11p15.5 spanning D11S1 through
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ACCESSION   AC001228 U90582
VERSION     AC001228.1  GI:1935053
KEYWORDS    HTG.
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 244254)
  AUTHORS   Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D.,
            Davie,J., Davies,C.J., Davis,C., English,C., Fondon,T.,
            Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O.,
            Hahner,L., Harris,J., Higgins,M., Hinson,S., Megarity,C.,
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            and Wilson,R.
  TITLE     Template
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 244254)
  AUTHORS   Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D.,
            Davie,J., Davies,C.J., Davis,C., English,C., Fondon,T.,
            Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O.,
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            and Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-APR-1997) Genome Science and Technology Center,
            University of Texas Southwestern Medical Center at Dallas, 5323
            Harry Hines Blvd, Dallas, TX 75235-8591, USA
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ORIGIN

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Qy   2015 ccttgcacggtggcagcacccccggcagcggcggccccccagagagggcggggcccaca 2074
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Qy   2135 ccctgcccacctacgagcagctgaccgtgcccaggaggggccccgatgaggggtcctgag 2194
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Qy   2255 ggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcaga 2314
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Qy   2375 gccacctcttcctggccggtgtgggggccccgtctcaggtctgagttgttaccccaagcg 2434
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Qy   2615 tccaggaccctgccaggcacaggcagggcaggaccagcccacgctgactacagggccacc 2674
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Qy   2855 ctgggttagactgccagctcttcctagctggagaggagccctgcctctccgcccctgagc 2914
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Qy   2915 ccactgtgcgtggggctcccgcctccaaccccctcgcccagtcccagcagccagccaaaca 2974
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Qy   3035 ctacacaggacaggggttccttctgggcattacatcgcatagaaatcaataatttgtggt 3094
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Qy   3155 ttttcctaataaacgtggagaatcaca 3181
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Db  28489 TTTTCCTAATAAACGTGGAGAATCACA 28515


RESULT   8
AC003693
LOCUS       AC003693   155074 bp    DNA             PRI       30-SEP-1998
DEFINITION  Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene,
            complete sequence.
ACCESSION   AC003693
VERSION     AC003693.1  GI:3687269
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 155074)
  AUTHORS   Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
            Buettner,J., Bumeister,R., Card,P., deSailboat,F., Dunn,J.,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
            Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
            Schageman,J., Schultz,R.A., Stimson,S., Syed,M. and Ward,T.
  TITLE     HTGS Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 155074)
  AUTHORS   Evans,G.A., Athanasiou,M., Basit,M., Bradbury,P., Brignac,S.,
            Bumesiter,R., Davis,C., English,C., Franklin,T.L., Garner,H.R.,
            Gee,V., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J.,
            Hinson,S., Narayanaswamy,U., Newton,J., O'Brien,K., Patel,P.,
            Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,
            Ward,T. and Wilson,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1997) Genome Science & Technology Center,
            University of Texas Southwester Medical Center, 5323 Harry Hines
            Blvd, Dallas, TX 75235-8591, USA
REFERENCE   3  (bases 1 to 155074)
  AUTHORS   Evans,G.A., Athanasiou,M., Aguayo,P., Armstrong,D., Basit,M.,
            Buettner,J., Butler,C., Card,P., deSailboat,F., Dunn,J.,
            English,C., Ethridge,S., Garner,H.R., Gee,V., Gordon,M., Gotway,G.,
            Grant,O., Hahner,L., Joslin,J., Lewis,E., Loo,H., Loo,K.N.,
            Major,T., McFarland,J., Newton,J., Osborne-Lawrence,S.,
            Schageman,J., Schultz,R.A., Stimson,S., Waller,K. and Ward,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-SEP-1998) Genome Science & Technology Center,
            University of Texas Southwestern Medical Center, 5323 Harry Hines
            Blvd, Dallas, TX 75235-8591, USA
COMMENT     On Oct 1, 1998 this sequence version replaced gi:3264564.
            Further information regarding the map of this region or
            annotation of pDJ915f1 can be found at
            http://gestec.swmed.edu/chromoso.htm
            IMPORTANT: This submission contains the entire insert of clone
            pDJ915f1.  pDJ915f1 comes from the RPCI-3 PAC library constructed
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at the Roswell Park Cancer Institute by the Pieter de Jong group. This clone has been finished according to strict quality criteria and attempts have been made to resolve all base calling problems such as compressions and repetitive elements. The expected Phred/Phrap calculated errors/10kb is 0.97. In addition, attempts have been made to assure over 99% of consensus base calls consist of either double-stranded coverage or 2 types of labeling chemistry on one strand.
CHROMOSOMAL LOCUS: This PAC clone comes from the Chromosome 11p15.5 Wilms tumor type 2 (WT2) region between ESTs CTSD and IGF2(INSL2). This region spanning approximately 2 Mbp is mapped between D11S2701 and D11S1145.
MARKER CONFIRMATION: STS WI-9248.

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repeat_region complement(26921. .27026)
/rpt_family="Alu"
repeat_region 32140. .32471
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/rpt_family="Alu"
repeat_region 39386. .39469
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/rpt_family="MLT1"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7e-276;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 59926 CTGCCCCCTCCGGCCCCGCCCCGAGCGCCCGGGCTGGGCCGGCAGCGGCCCCCCGCGGCG 59985

Qy 61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120

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Db  59986 GGGCTGGCAGCAGTGGCTGCCCGCACTGCGCCCGGGCGCTCGCCTTCGCTGCAGCTCCCG 60045

Qy    121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180
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Db  60046 GTGCCGCCGCTCGGGCCGGCCCCCCGGCAGGCCCTCCTCGTTATGGCCGCGGCCTCCTCC 60105

Qy    181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240
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Db  60106 CCGCCCAGGGCCGAGAGGAAGCGCTGGGGTTGGGGCCGCCTGCCAGGCGCCCGGCGGGGC 60165

Qy    241 agcgcgggcctggccaagaagtgccccttctcgctggagctggcggagggcggcccggcg 300
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Db  60166 AGCGCGGGCCTGGCCAAGAAGTGCCCCTTCTCGCTGGAGCTGGCGGAGGGCGGCCCGGCG 60225

Qy    301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgcccccctgcgtcc 360
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Db  60286 CCGGCCGCGCCCGCCGCGCCCCCAGTTGCCTCCGACCTTGGCCCGCGGCCGCCGGTGAGC 60345

Qy    421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480
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Qy    481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540
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Qy    541 ttcgccgt 548
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RESULT  9
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LOCUS       AB01514S02    471 bp    DNA             PRI       14-APR-2000
DEFINITION  Homo sapiens KVLQT1 gene for potassium channel subunit, exon 1a.
ACCESSION   AB015148
VERSION     AB015148.1  GI:3953621
KEYWORDS    KVLQT1.
SEGMENT     2 of 17
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Itoh,T., Tanaka,T., Nagai,R., Kikuchi,K., Ogawa,S., Okada,S.,
            Yamagata,S., Yano,K., Yazaki,Y. and Nakamura,Y.
  TITLE     Genomic organization and mutational analysis of KVLQT1, a gene
            responsible for familial long QT syndrome
  JOURNAL   Hum. Genet. 103 (3), 290-294 (1998)
  MEDLINE   99013427
REFERENCE   2  (bases 1 to 471)
  AUTHORS   Tanaka,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1998) to the DDBJ/EMBL/GenBank databases.
            Toshihiro Tanaka, Institute of Medical Science, University of
            Tokyo, Laboratory of Molecular Medicine; 4-6-1 Shirokanedai,
            Minato-ku, Tokyo 108-8639, Japan
            (E-mail:toshitan@ims.u-tokyo.ac.jp, Tel:81-3-5449-5374,
            Fax:81-3-5449-5406)
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Qy    520 tggaaatgcttcgtttaccacttcgccgt 548
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RESULT  10
HSU86146
LOCUS       HSU86146      386 bp    mRNA            PRI       10-MAY-1997
DEFINITION  Human voltage-gated potassium channel KvLQT1 (KVLQT1) mRNA, partial
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ACCESSION   U86146
VERSION     U86146.1  GI:2076879
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 386)
  AUTHORS   Yang,W.P., Levesque,P.C., Little,W.A., Conder,M.L., Shalaby,F.Y.
            and Blanar,M.A.
  TITLE     KvLQT1, a voltage-gated potassium channel responsible for human
            cardiac arrhythmias
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4017-4021 (1997)
  MEDLINE   97268689
REFERENCE   2  (bases 1 to 386)
  AUTHORS   Yang,W.P., Levesque,P.C., Little,W.A., Conder,M.L., Shalaby,F.Y.
            and Blanar,M.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-JAN-1997) Cardiovascular Drug Discovery,
            Bristol-Myers Squibb PRI, K14-01, P.O. Box 4000, Princeton, NJ
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ORIGIN


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Qy    223 ccaggcgcccggcggggcagcgcgggcctggccaagaagtgccccttctcgctggagctg 282
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Qy    283 gcggagggcggcccggcgggcggcgcgctctacgcgcccatcgcgcccggcgccccaggt 342
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Qy    343 cccgcgccccctgcgtccccggccgcgcccgccgcgcccccagttgcctccgaccttggc 402
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Qy    463 ttggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggctgg 522
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Db    301 TTGGCGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCCTCGAGCGTCCCACCGGCTGG 360

Qy    523 aaatgcttcgtttaccacttcgccgt 548
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Db    361 AAATGCTTCGTTTACCACTTCGCCGT 386


RESULT  11
AB01514S17
LOCUS       AB01514S17    298 bp    DNA             PRI       14-APR-2000
DEFINITION  Homo sapiens KVLQT1 gene for potassium channel subunit, exon 15 and
            complete cds.
ACCESSION   AB015163
VERSION     AB015163.1  GI:3953682
KEYWORDS    KVLQT1 isoform1; KVLQT1 isoform2.
SEGMENT     17 of 17
SOURCE      Homo sapiens DNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Itoh,T., Tanaka,T., Nagai,R., Kikuchi,K., Ogawa,S., Okada,S.,
            Yamagata,S., Yano,K., Yazaki,Y. and Nakamura,Y.
  TITLE     Genomic organization and mutational analysis of KVLQT1, a gene
            responsible for familial long QT syndrome
  JOURNAL   Hum. Genet. 103 (3), 290-294 (1998)
  MEDLINE   99013427
REFERENCE   2  (bases 1 to 298)
  AUTHORS   Tanaka,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1998) to the DDBJ/EMBL/GenBank databases.
            Toshihiro Tanaka, Institute of Medical Science, University of
            Tokyo, Laboratory of Molecular Medicine; 4-6-1 Shirokanedai,
            Minato-ku, Tokyo 108-8639, Japan
            (E-mail:toshitan@ims.u-tokyo.ac.jp, Tel:81-3-5449-5374,
            Fax:81-3-5449-5406)
FEATURES             Location/Qualifiers
     source          1. .298
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                     /chromosome="11"
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                     AB015150.1:20. .146,AB015151.1:63. .141,AB015152.1:24. .120,
                     AB015153.1:35. .175,AB015154.1:29. .139,AB015155.1:50. .145,
                     AB015156.1:39. .161,AB015157.1:50. .191,AB015158.1:38. .158,
                     AB015159.1:41. .116,AB015160.1:39. .133,AB015161.1:80. .126,
                     AB015162.1:84. .145,23. .259)
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                     AB015156.1:39. .161,AB015157.1:50. .191,AB015158.1:38. .158,
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                     AB015162.1:84. .145,23. .259)
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                     HHRATIKVIRRMQYFVAKKKFQQARKPYDVRDVIEQYSQGHLNLMVRIKELQRRLDQS
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                     PGSGGPPREGGAHITQPCGSGGSVDPELFLPSNTLPTYEQLTVPRRGPDEGS"
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                     AB015156.1:39. .161,AB015157.1:50. .191,AB015158.1:38. .158,
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                     AB015156.1:39. .161,AB015157.1:50. .191,AB015158.1:38. .158,
                     AB015159.1:41. .116,AB015160.1:39. .133,AB015161.1:80. .126,
                     AB015162.1:84. .145,23. .259)
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                     IRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLAEKDA
                     VNESGRVEFGSYADALWWGVVTVTTIGYGDKVPQTWVGKTIASCFSVFAISFFALPAG
                     ILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSSTWKIYIRKAPRSH
                     TLLSPSPKPKKSVVVKKKKFKLDKDNGVTPGEKMLTVPHITCDPPEERRLDHFSVDGY
                     DSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPITHISQLREHHRATIKVIRR
                     MQYFVAKKKFQQARKPYDVRDVIEQYSQGHLNLMVRIKELQRRLDQSIGKPSLFISVS
                     EKSKDRGSNTIGARLNRVEDKVTQLDQRLALITDMLHQLLSLHGGSTPGSGGPPREGG
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  Matches  278;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1955 aggtgacgcagctggaccagaggctggcactcatcaccgacatgcttcaccagctgctct 2014
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Db      21 AGGTGACGCAGCTGGACCAGAGGCTGGCACTCATCACCGACATGCTTCACCAGCTGCTCT 80

Qy    2015 ccttgcacggtggcagcacccccggcagcggcggcccccccagagagggcggggcccaca 2074
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      81 CCTTGCACGGTGGCAGCACCCCCGGCAGCGGCGGCCCCCCCAGAGAGGGCGGGGCCCACA 140

Qy    2075 tcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaaca 2134
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Db     141 TCACCCAGCCCTGCGGCAGTGGCGGCTCCGTCGACCCTGAGCTCTTCCTGCCCAGCAACA 200

Qy    2135 ccctgcccacctacgagcagctgaccgtgcccaggaggggcccccgatgaggggtcctgag 2194
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Db     201 CCCTGCCCACCTACGAGCAGCTGACCGTGCCCAGGAGGGGCCCCGATGAGGGGTCCTGAG 260

Qy    2195 gaggggatggggctgggggatgggcctgagtgagaggg 2232
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Db     261 GAGGGGATGGGGCTGGGGGATGGGCCTGAGTGAGAGGG 298


RESULT  12
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WPCOMMENT
  Sequence split into 4 fragments  LOCUS HSA6345 Accession AJ006345
     Fragment Name      Begin     End
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     HSA6345_1         100001    210000
     HSA6345_2         200001    310000
     HSA6345_3         300001    404123
LOCUS       HSA6345    404123 bp    DNA             PRI       15-JUN-1999
DEFINITION  Homo sapiens KVLQT1 gene.
ACCESSION   AJ006345
VERSION     AJ006345.1  GI:5042384
KEYWORDS    KvLQT1 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 404123)
  AUTHORS   Neyroud,N., Richard,P., Vignier,N., Donger,C., Denjoy,I., Demay,L.,
            Shkolnikova,M., Pesce,R., Hainque,B., Coumel,P., Schwartz,K. and
            Guicheney,P.
  TITLE     Genomic organization of the KCNQ1 K+ channel gene and
            identification of C-terminal mutations in the long-QT syndrome
  JOURNAL   Circ. Res. 84 (3), 290-297 (1999)
  MEDLINE   99147971
REFERENCE   2  (bases 1 to 323655; 1 to 323655)
  AUTHORS   Neyroud,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAY-1998) Neyroud N., Institut de Myologie, INSERM
            U153, 47 Boulevard de l'Hopital, Paris RL 75013, France
FEATURES             Location/Qualifiers
     source          1. .404123
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                     /db_xref="taxon:9606"
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     5'UTR           893. .1000
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                     127222. .127300,127910. .128006,128743. .128883,
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                     IVLVVFFXTEYVVRLWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVASMVVLCVGSK
                     GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFS
                     SYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIGYGDKVPQTWVGKTIASCFSV
                     FAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSSTW
                     KIYIRKAPRSHTLLSPSPKPKKSVVVKKKKFKLDKDNGVTPGEKMLTVPHITCDPPEE
                     RRLDHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLEGETLLTPITHISQLRE
                     HHRATIKVIRRMQYFVAKKKFQQARKPYDVRDVIEQYSQGHLNLMVRIKELQRRLDQS
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                     /note="1a"
                     /number=1
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                     /note="isoform 2, isoform 3, isoform 4"
     misc_RNA        join(17612. .17616,77400. .77491,83848. .83938,
                     119671. .119933,126525. .126651,127222. .127300,
                     127910. .128006,128743. .128883,139334. .139444,
                     141113. .141208,143472. .143594,144615. .144756,
                     217008. .217128,323883. .323958,330963. .331057,
                     331989. .332035,332980. .333041,402674. .402910)
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                     /note="isoform 4; RNA transcribed but not translated"
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                     128743. .128883,139334. .139444,141113. .141208,
                     143472. .143594,144615. .144756,217008. .217128,
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                     127222. .127300,127910. .128006,128743. .128883,
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                     402674. .402910)
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                     TLLSPSPKPKKSVVVKKKKFKLDKDNGVTPGEKMLTVPHITCDPPEERRLDHFSVDGY
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                     /note="1b"
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ORIGIN


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Db    839 CTGCCCCCTCCGGCCCCGCCCCGAGCGCCCGGGCTGGGCCGGCAGCGGCCCCCCGCGGCG 898

Qy     61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120
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Db    899 GGGCTGGCAGCAGTGGCTGCCCGCACTGCGCCCGGGCGCTCGCCTTCGCTGCAGCTCCCG 958

Qy    121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180
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Qy    181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240
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Db   1019 CCGCCCAGGGCCGAAAGGAAGCGCTGGGGTTGGGGCCGCCTGCCAGGCGCCCGGCGGGGC 1078

Qy    241 agcgcgggcctggccaa 257
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Db   1079 AGCGCGGGCCTGGCCAA 1095


RESULT  13
AF003743
LOCUS       AF003743      304 bp    mRNA            PRI       03-FEB-1998
DEFINITION  Homo sapiens delayed rectifier potassium channel (KVLQT1-Iso5)
            mRNA, 5' UTR and partial cds.
ACCESSION   AF003743
VERSION     AF003743.1  GI:2198821
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 304)
  AUTHORS   Wollnik,B., Schroeder,B.C., Kubisch,C., Esperer,H.D., Wieacker,P.
            and Jentsch,T.J.
  TITLE     Pathophysiological mechanisms of dominant and recessive KVLQT1 K+
            channel mutations found in inherited cardiac arrhythmias
  JOURNAL   Hum. Mol. Genet. 6 (11), 1943-1949 (1997)
  MEDLINE   98027069
REFERENCE   2  (bases 1 to 304)
  AUTHORS   Wollnik,B., Schroeder,B., Kubisch,C., Esperer,H.D., Wieacker,P. and
            Jentsch,T.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-MAY-1997) Center for Molecular Neurobiology (ZMNH),
            Martinistrasse 85, Hamburg 20246, Germany
FEATURES             Location/Qualifiers
     source          1. .304
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                     /db_xref="taxon:9606"
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     5'UTR           <1. .139
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                     /note="exon 1a2"
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                     /note="delayed rectifier potassium channel KVLQT1"
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                     /protein_id="AAC00066.1"
                     /db_xref="GI:2198822"
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     exon            164. .255
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                     /note="exon 1c"
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ORIGIN


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  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    386 ttgcctccgaccttggcccgcggccgccggtgagcctagacccgcgcgtctccatctaca 445
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Db      1 TTGCCTCCGACCTTGGCCCGCGGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACA 60
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Qy    446 gcacgcgccgcccggtgttggcgcgcacccacgtccagggccgcgtctacaacttcctcg 505
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Db     61 GCACGCGCCGCCCGGTGTTGGCGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCCTCG 120

Qy    506 agcgtcccaccggctggaaatgcttcgtttaccacttcgccgt 548
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Db    121 AGCGTCCCACCGGCTGGAAATGCTTCGTTTACCACTTCGCCGT 163


RESULT  14
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LOCUS       AC026645   160847 bp    DNA             HTG       01-SEP-2000
DEFINITION  Homo sapiens chromosome 11 clone RP11-113A6, WORKING DRAFT
            SEQUENCE, 29 unordered pieces.
ACCESSION   AC026645
VERSION     AC026645.4  GI:9958138
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 160847)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 160847)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Sep 1, 2000 this sequence version replaced gi:8348019.

            ----------------- Genome Center -----------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            -------------- Project Information --------------
            Center project name: H_NH0113A06
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 97% of reads
            Chemistry: Dye-terminator Big Dye; 3% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 137493 bases at least Q40
            Consensus quality: 145360 bases at least Q30
            Consensus quality: 149518 bases at least Q20
            Insert size: 152000; agarose-fp
            Insert size: 158047; sum-of-contigs
            Quality coverage: 3.70 in Q20 bases; agarose-fp
            Quality coverage: 3.66 in Q20 bases; sum-of-contigs
            ---------------------------------------------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 29 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1509: contig of 1509 bp in length
            *     1510     1609: gap of unknown length
            *     1610     3508: contig of 1899 bp in length
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            *    17999    19740: contig of 1742 bp in length
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            *    19841    21377: contig of 1537 bp in length
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DEFINITION  Homo sapiens KVLQT1 gene for potassium channel subunit, exon 5.
ACCESSION   AB015153
VERSION     AB015153.1  GI:3953626
KEYWORDS    KVLQT1.
SEGMENT     7 of 17
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Itoh,T., Tanaka,T., Nagai,R., Kikuchi,K., Ogawa,S., Okada,S.,
            Yamagata,S., Yano,K., Yazaki,Y. and Nakamura,Y.
  TITLE     Genomic organization and mutational analysis of KVLQT1, a gene
            responsible for familial long QT syndrome
  JOURNAL   Hum. Genet. 103 (3), 290-294 (1998)
  MEDLINE   99013427
REFERENCE   2  (bases 1 to 237)
  AUTHORS   Tanaka,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1998) to the DDBJ/EMBL/GenBank databases.
            Toshihiro Tanaka, Institute of Medical Science, University of
            Tokyo, Laboratory of Molecular Medicine; 4-6-1 Shirokanedai,
            Minato-ku, Tokyo 108-8639, Japan
            (E-mail:toshitan@ims.u-tokyo.ac.jp, Tel:81-3-5449-5374,
            Fax:81-3-5449-5406)
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Search completed: November  2, 2001, 13:12:48
Job time: 4179 sec
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GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 13:12:54 ; Search time 892.35 Seconds
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Perfect score: 3181
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3065065 seqs, 1406758252 residues

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Total number of hits satisfying chosen parameters: 561151

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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US-09-880-107-3358
; Sequence 3358, Application US/09880107
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3358
; LENGTH: 2821
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U40990
US-09-880-107-3358

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RESULT   2
US-60-313-371-1495
; Sequence 1495, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
;  SOFTWARE: PERL Program
; SEQ ID NO 1495
;   LENGTH: 2924
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:NM_000218
US-60-313-371-1495


  Query Match            84.9%;  Score 2702;  DB 10;  Length 2924;
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Qy    660 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtggg 719
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2803 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 2862

Qy   3120 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2863 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 2922

Qy   3180 ca 3181
          ||
Db   2923 ca 2924
```

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RESULT   3
US-60-324-185-25008
; Sequence 25008, Application US/60324185
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE: GX-0019-1 P
;  CURRENT APPLICATION NUMBER: US/60/324,185
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 35862
;  SOFTWARE: PERL Program
; SEQ ID NO 25008
;   LENGTH: 4833
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 348127.7
US-60-324-185-25008
```

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  Query Match             83.3%;  Score 2651;  DB 10;  Length 4833;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2701;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    480 ccagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttacca 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116 ccagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttacca 2175

Qy    540 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 2235

Qy    600 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 2295

Qy    660 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtggg 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtggg 2355

Qy    720 cctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356 cctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 2415

Qy    780 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 2475

Qy    840 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   2476 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 2535

Qy    900 cacctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccct 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536 cacctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccct 2595

Qy    960 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 2655

Qy   1020 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2656 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 2715

Qy   1080 ggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaa 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2716 ggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaa 2775

Qy   1140 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 2835

Qy   1200 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2836 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 2895

Qy   1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2896 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 2955

Qy   1320 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2956 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 3015

Qy   1380 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3016 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 3075

Qy   1440 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3076 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 3135

Qy   1500 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3136 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 3195

Qy   1560 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3196 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 3255

Qy   1620 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3256 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 3315

Qy   1680 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3316 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 3375

Qy   1740 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3376 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 3435

Qy   1800 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3436 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 3495

Qy   1860 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3496 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 3555

Qy   1920 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3556 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 3615
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Qy   1980 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3616 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 3675

Qy   2040 cagcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3676 cagcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 3735

Qy   2100 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3736 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 3795

Qy   2160 cgtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggc 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3796 cgtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggc 3855

Qy   2220 ctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctc 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3856 ctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctc 3915

Qy   2280 ctaaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgc 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3916 ctaaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgc 3975

Qy   2340 tgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtggg 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2400 ggccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttg 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4036 ggccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttg 4095

Qy   2460 acatcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatgg 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4096 acatcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatgg 4155

Qy   2520 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgag 2579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4156 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgag 4215

Qy   2580 gggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggca 2639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4216 gggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggca 4275

Qy   2640 gggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatt 2699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4276 gggcaggaccagcccacgctgactacagggccgccggcaataaaagcccaggagcccatt 4335

Qy   2700 tggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagact 2759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4336 tggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagact 4395

Qy   2760 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttcccca 2819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4396 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttcccca 4455

Qy   2820 gggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcct 2879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4456 gggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcct 4515

Qy   2880 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4516 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 4575

Qy   2940 caaccccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4576 caaccccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 4635

Qy   3000 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4636 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 4695
```

```
Qy   3060 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4696 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 4755

Qy   3120 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4756 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 4815

Qy   3180 ca 3181
          ||
Db   4816 ca 4817
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RESULT 4
US-60-313-371-1500
; Sequence 1500, Application US/60313371
; GENERAL INFORMATION:
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Malsen, Gareth
; APPLICANT: Townley, David
; APPLICANT: Morris, MacDonald
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
; FILE REFERENCE: GX-0013-5 P
; CURRENT APPLICATION NUMBER: US/60/313,371
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 2447
; SOFTWARE: PERL Program
; SEQ ID NO 1500
; LENGTH: 2702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: KCNQ1_mrna_build.1
US-60-313-371-1500

Query Match 82.2%; Score 2615; DB 10; Length 2702;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2665; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    484 ggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccacttc 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     37 ggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccacttc 96

Qy    544 gccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcag 603
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     97 gccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcag 156

Qy    604 tatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttcttc 663
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    157 tatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttcttc 216

Qy    664 gggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcctc 723
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    217 sggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcctc 276

Qy    724 tgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtg 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 tgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtg 336

Qy    784 gcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggccatc 843
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    337 gcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggccatc 396

Qy    844 aggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggcacc 903
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    397 aggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggcacc 456

Qy    904 tggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctgtac 963
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    964 atcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggacgcg 1023
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Db    517 atcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggacgcg 576

Qy   1024 gtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggggtg 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    577 gtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggggtg 636

Qy   1084 gtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaagacc 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 gtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaagacc 696

Qy   1144 atcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggattctt 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    697 atcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggattctt 756

Qy   1204 ggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccggcag 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 ggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccggcag 816

Qy   1264 atcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaacccc 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 atcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaacccc 876

Qy   1324 gactcctccacctggaagatctacatccggaaggccccccggagccacactctgctgtca 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 gactcctccacctggaagatctacatccggaaggccccccggagccacactctgctgtca 936

Qy   1384 cccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggacaaa 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 cccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggacaaa 996

Qy   1444 gacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgacccc 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 gacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgacccc 1056

Qy   1504 ccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaaggaag 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 ccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaaggaag 1116

Qy   1564 agcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgccgag 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 agcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgccgag 1176

Qy   1624 gacctggacctggaaggggagactctgctgacacccatcacccacatctcacagctgcgg 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 gacctggacctggaaggggagactctgctgacacccatcacccacatctcacagctgcgg 1236

Qy   1684 gaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaagaag 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 gaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaagaag 1296

Qy   1744 aaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcgcag 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 aaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcgcag 1356

Qy   1804 ggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtccatt 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 ggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtccatt 1416

Qy   1864 gggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacg 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 gggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacg 1476

Qy   1924 atcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctggca 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 atcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctggca 1536

Qy   1984 ctcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccggcagc 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1537 ctcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccggcagc 1596

Qy   2044 ggcggccccccccagagagggcggggcccacatcacccagccctgcggcagtggcggctcc 2103
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Db   1597 ggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcggctcc 1656

Qy   2104 gtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtg 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1657 gtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtg 1716

Qy   2164 cccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcctga 2223
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1717 cccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcctga 1776

Qy   2224 gtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctcctaa 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1777 gtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctcctaa 1836

Qy   2284 aaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgctgtc 2343
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Db   1837 aaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgctgtc 1896

Qy   2344 tggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggggcc 2403
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1897 tggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggggcc 1956

Qy   2404 ccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttgacat 2463
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1957 ccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttgacat 2016

Qy   2464 cactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggccag 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2017 cactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggccag 2076

Qy   2524 gaagtagcacaggctgagtgcaggcccaccctgcttggcccagggggcttcctgagggga 2583
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2077 gaagtagcacaggctgagtgcaggcccaccctgcttggcccagggggcttcctgagggga 2136

Qy   2584 gacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcagggc 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2137 gacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcagggc 2196

Qy   2644 aggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatttgga 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2197 aggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatttgga 2256

Qy   2704 gggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactgtgg 2763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2257 gggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactgtgg 2316

Qy   2764 agactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccagggc 2823
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2317 agactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccagggc 2376

Qy   2824 acgtggttgagtgggggaacgcccacttccctgggttagactgccagctcttcctagct 2883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2377 acgtggttgagtgggggaacgcccacttccctgggttagactgccagctcttcctagct 2436

Qy   2884 ggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctccaac 2943
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2437 ggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctccaac 2496

Qy   2944 ccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctccccttgc 3003
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2497 ccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctccccttgc 2556

Qy   3004 cagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgggca 3063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2557 cagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgggca 2616

Qy   3064 ttacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagtttca 3123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2617 ttacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagtttca 2676

Qy   3124 cagtgtgattttgattattaattgtg 3149
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Db   2677 cagtgtgattttgattattaattgtg 2702
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RESULT 5
US-60-313-371-1496
; Sequence 1496, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
;  SOFTWARE: PERL Program
; SEQ ID NO 1496
;   LENGTH: 1746
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:NM_000218.1
US-60-313-371-1496


  Query Match             53.9%;  Score 1714;  DB 10;  Length 1746;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1714;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    480 ccagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttacca 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     33 ccagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttacca 92

Qy    540 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     93 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 152

Qy    600 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    153 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 212

Qy    660 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtggg 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    213 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtggg 272

Qy    720 cctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    273 cctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 332

Qy    780 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    333 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 392

Qy    840 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 452

Qy    900 cacctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccct 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 cacctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccct 512

Qy    960 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    513 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 572

Qy   1020 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    573 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 632

Qy   1080 ggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaa 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    633 ggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaa 692

Qy   1140 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 752

Qy   1200 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 812

Qy   1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 872

Qy   1320 ccccgactcctccacctggaagatctacatccggaaggcccccccggagccacactctgct 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 ccccgactcctccacctggaagatctacatccggaaggcccccccggagccacactctgct 932

Qy   1380 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 992

Qy   1440 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1052

Qy   1500 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1112

Qy   1560 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1172

Qy   1620 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1232

Qy   1680 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1292

Qy   1740 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1352

Qy   1800 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1412

Qy   1860 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1472

Qy   1920 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1532

Qy   1980 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 2039
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Qy   2040 cagcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1593 cagcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 1652

Qy   2100 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 2159
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Db   1653 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 1712

Qy   2160 cgtgcccaggaggggccccgatgaggggtcctga 2193
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US-60-313-371-1499
; Sequence 1499, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
;  SOFTWARE: PERL Program
; SEQ ID NO 1499
;   LENGTH: 1746
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: KCNQ1_cds.1
US-60-313-371-1499


  Query Match             52.2%;  Score 1659;  DB 10;  Length 1746;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1709;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db     37 ggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccacttc 96

Qy    544 gccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcag 603
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Db     97 gccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcag 156

Qy    604 tatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttcttc 663
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Qy    664 gggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcctc 723
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Qy    724 tgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtg 783
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    277 tgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtg 336

Qy    784 gcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggccatc 843
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Qy    844 aggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggcacc 903
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Qy    904 tggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctgtac 963
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Db    457 tggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctgtac 516

Qy    964 atcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggacgcg 1023
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    517 atcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggacgcg 576

Qy   1024 gtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggggtg 1083
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1084 gtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaagacc 1143
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    637 gtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaagacc 696
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Qy   1144 atcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggattctt 1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1204 ggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccggcag 1263
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    757 ggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccggcag 816

Qy   1264 atcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaacccc 1323
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    817 atcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaacccc 876

Qy   1324 gactcctccacctggaagatctacatccggaaggccccccggagccacactctgctgtca 1383
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    877 gactcctccacctggaagatctacatccggaaggccccccggagccacactctgctgtca 936

Qy   1384 cccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggacaaa 1443
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    937 cccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggacaaa 996

Qy   1444 gacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgacccc 1503
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    997 gacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgacccc 1056

Qy   1504 ccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaaggaag 1563
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1057 ccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaaggaag 1116

Qy   1564 agcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgccgag 1623
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1117 agcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgccgag 1176

Qy   1624 gacctggacctggaaggggagactctgctgacacccatcacccacatctcacagctgcgg 1683
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1177 gacctggacctggaaggggagactctgctgacacccatcacccacatctcacagctgcgg 1236

Qy   1684 gaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaagaag 1743
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1237 gaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaagaag 1296

Qy   1744 aaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcgcag 1803
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1297 aaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcgcag 1356

Qy   1804 ggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtccatt 1863
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1357 ggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtccatt 1416

Qy   1864 gggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacg 1923
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1417 gggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacg 1476

Qy   1924 atcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctggca 1983
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1477 atcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctggca 1536

Qy   1984 ctcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcaccccggcagc 2043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1537 ctcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcaccccggcagc 1596

Qy   2044 ggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcggctcc 2103
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1597 ggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcggctcc 1656

Qy   2104 gtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtg 2163
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1657 gtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtg 1716

Qy   2164 cccaggaggggccccgatgaggggtcctga 2193
          |||||||||||||||||||||||||||||
Db   1717 cccaggaggggccccgatgaggggtcctga 1746
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RESULT 7
US-60-324-185-25008/c
; Sequence 25008, Application US/60324185
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT:  Lal, Preeti
;  APPLICANT:  Diep, Dinh
;  TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS IDENTIFIED THEREBY
;  FILE REFERENCE: GX-0019-1 P
;  CURRENT APPLICATION NUMBER: US/60/324,185
;  CURRENT FILING DATE:  2001-09-21
;  NUMBER OF SEQ ID NOS: 35862
;  SOFTWARE: PERL Program
; SEQ ID NO 25008
;   LENGTH: 4833
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 348127.7
US-60-324-185-25008
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Query Match 51.5%; Score 1637; DB 10; Length 4833;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1877; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Qy    549 cttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcagtatgc 608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1883 CTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGTGCTGTCCACCATCGAGCAGTATGC 1824

Qy    609 cgccctggccacggggactctcttctggatggagatcgtgctggtggtgttcttcgggac 668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1823 CGCCCTGGCCACGGGGACTCTCTTCTGGATGGAGATCGTGCTGGTGGTGTTCTTCGGGAC 1764

Qy    669 ggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcctctgggg 728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1763 GGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCGCAGCAAGTACGTGGGCCTCTGGGG 1704

Qy    729 gcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtggcctc 788
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1703 GCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCATCGACCTCATCGTGGTCGTGGCCTC 1644

Qy    789 catggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggccatcagggg 848
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1643 CATGGTGGTCCTCTGCGTGGGCTCCAAGGGGCAGGTGTTTGCCACGTCGGCCATCAGGGG 1584

Qy    849 catccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggcacctggag 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1583 CATCCGCTTCCTGCAGATCCTGAGGATGCTACACGTCGACCGCCAGGGAGGCACCTGGAG 1524

Qy    909 gctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctgtacatcgg 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1523 GCTCCTGGGCTCCGTGGTCTTCATCCACCGCCAGGAGCTGATAACCACCCTGTACATCGG 1464

Qy    969 cttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggacgcggtgaa 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1463 CTTCCTGGGCCTCATCTTCTCCTCGTACTTTGTGTACCTGGCTGAGAAGGACGCGGTGAA 1404

Qy   1029 cgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggggggtggtcac 1088
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1403 CGAGTCAGGCCGCGTGGAGTTCGGCAGCTACGCAGATGCGCTGTGGTGGGGGGTGGTCAC 1344

Qy   1089 agtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaagaccatcgc 1148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1343 AGTCACCACCATCGGCTATGGGGACAAGGTGCCCCAGACGTGGGTCGGGAAGACCATCGC 1284

Qy   1149 ctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggattcttggctc 1208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1283 CTCCTGCTTCTCTGTCTTTGCCATCTCCTTCTTTGCGCTCCCAGCGGGGATTCTTGGCTC 1224
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Qy   1209 ggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccggcagatccc 1268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1223 GGGGTTTGCCCTGAAGGTGCAGCAGAAGCAGAGGCAGAAGCACTTCAACCGGCAGATCCC 1164

Qy   1269 ggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaaccccgactc 1328
          ||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1163 GGCG---GCCTCACTCATTCAGACCGCATGGAGGTGCTATGCTGCCGAGAACCCCGACTC 1107

Qy   1329 ctccacctggaagatctacatccggaaggccccccggagccacactctgctgtcacccag 1388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1106 CTCCACCTGGAAGATCTACATCCGGAAGGCCCCCCGGAGCCACACTCTGCTGTCACCCAG 1047

Qy   1389 ccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggacaaagacaa 1448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1046 CCCCAAACCCAAGAAGTCTGTGGTGGTAAAGAAAAAAAAGTTCAAGCTGGACAAAGACAA 987

Qy   1449 tggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgacccccccaga 1508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    986 TGGGGTGACTCCTGGAGAGAAGATGCTCACAGTCCCCCATATCACGTGCGACCCCCCAGA 927

Qy   1509 agagcggcggctggaccacttctctgtcgacggctatgacagttctgtaaggaagagccc 1568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    926 AGAGCGGCGGCTGGACCACTTCTCTGTCGACGGCTATGACAGTTCTGTAAGGAAGAGCCC 867

Qy   1569 aacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgccgaggacct 1628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    866 AACACTGCTGGAAGTGAGCATGCCCCATTTCATGAGAACCAACAGCTTCGCCGAGGACCT 807

Qy   1629 ggacctggaaggggagactctgctgacacccatcacccacatctcacagctgcgggaaca 1688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    806 GGACCTGGAAGGGGAGACTCTGCTGACACCCATCACCCACATCTCACAGCTGCGGGAACA 747

Qy   1689 ccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaagaagaaatt 1748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    746 CCATCGGGCCACCATTAAGGTCATTCGACGCATGCAGTACTTTGTGGCCAAGAAGAAATT 687

Qy   1749 ccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcgcagggcca 1808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    686 CCAGCAAGCGCGGAAGCCTTACGATGTGCGGGACGTCATTGAGCAGTACTCGCAGGGCCA 627

Qy   1809 cctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtccattgggaa 1868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    626 CCTCAACCTCATGGTGCGCATCAAGGAGCTGCAGAGGAGGCTGGACCAGTCCATTGGGAA 567

Qy   1869 gccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacgatcgg 1928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    566 GCCCTCACTGTTCATCTCCGTCTCAGAAAAGAGCAAGGATCGCGGCAGCAACACGATCGG 507

Qy   1929 cgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctggcactcat 1988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    506 CGCCCGCCTGAACCGAGTAGAAGACAAGGTGACGCAGCTGGACCAGAGGCTGGCACTCAT 447

Qy   1989 caccgacatgcttcaccagctgctctccttgcacggtggcagcacccccggcagcggcgg 2048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    446 CACCGACATGCTTCACCAGCTGCTCTCCTTGCACGGTGGCAGCACCCCCGGCAGCGGCGG 387

Qy   2049 ccccccccagagagggcggggcccacatcacccagccctgcggcagtggcggctccgtcga 2108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    386 CCCCCCCAGAGAGGGCGGGGCCCACATCACCCAGCCCTGCGGCAGTGGCGGCTCCGTCGA 327

Qy   2109 ccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtgcccag 2168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    326 CCCTGAGCTCTTCCTGCCCAGCAACACCCTGCCCACCTACGAGCAGCTGACCGTGCCCAG 267

Qy   2169 gaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcctgagtgag 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    266 GAGGGGCCCCGATGAGGGGTCCTGAGGAGGGGATGGGGCTGGGGGATGGGCCTGAGTGAG 207

Qy   2229 aggggaggccaagagtggccccacctggccctctctgaaggaggccacctcctaaaaggc 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    206 AGGGGAGGCCAAGAGTGGCCCCACCTGGCCCTCTCTGAAGGAGGCCACCTCCTAAAAGGC 147
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Qy   2289 ccagagagaagagccccactctcagaggccccaataccccatggaccatgctgtctggca 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    146 CCAGAGAGAAGAGCCCCACTCTCAGAGGCCCCAATACCCCATGGACCATGCTGTCTGGCA 87

Qy   2349 cagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggggccccgtc 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     86 CAGCCTGCACTTGGGGGCTCAGCAAGGCCACCTCTTCCTGGCCGGTGTGGGGGCCCCGTC 27

Qy   2409 tcaggtctgagttgttaccc 2428
          ||||||||||||||||||||
Db     26 TCAGGTCTGAGTTGTTACCC 7


RESULT 8
US-60-313-371-1498
; Sequence 1498, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
;  SOFTWARE: PERL Program
; SEQ ID NO 1498
;   LENGTH: 404123
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AJ006345_1
US-60-313-371-1498


  Query Match             38.6%;  Score 1227;  DB 10;  Length 404123;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1955 aggtgacgcagctggaccagaggctggcactcatcaccgacatgcttcaccagctgctct 2014
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402672 aggtgacgcagctggaccagaggctggcactcatcaccgacatgcttcaccagctgctct 402731

Qy   2015 ccttgcacggtggcagcacccccggcagcggcggcccccccagagagggcggggcccaca 2074
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402732 ccttgcacggtggcagcacccccggcagcggcggcccccccagagagggcggggcccaca 402791

Qy   2075 tcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaaca 2134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402792 tcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaaca 402851

Qy   2135 ccctgcccacctacgagcagctgaccgtgcccaggaggggccccgatgaggggtcctgag 2194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402852 ccctgcccacctacgagcagctgaccgtgcccaggaggggccccgatgaggggtcctgag 402911

Qy   2195 gaggggatggggctgggggatgggcctgagtgagaggggaggccaagagtggccccacct 2254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402912 gaggggatggggctgggggatgggcctgagtgagaggggaggccaagagtggccccacct 402971

Qy   2255 ggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcaga 2314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 402972 ggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcaga 403031

Qy   2315 ggccccaataccccatggaccatgctgtctggcacagcctgcacttgggggctcagcaag 2374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2375 gccacctcttcctggccggtgtgggggccccgtctcaggtctgagttgttaccccaagcg 2434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403092 gccacctcttcctggccggtgtgggggccccgtctcaggtctgagttgttaccccaagcg 403151
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Qy   2435 ccctggcccccacatggtgatgttgacatcactggcatggtggttgggacccagtggcag 2494
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Db 403152 ccctggcccccacatggtgatgttgacatcactggcatggtggttgggacccagtggcag 403211

Qy   2495 ggcacagggcctggcccatgtatggccaggaagtagcacaggctgagtgcaggcccaccc 2554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403212 ggcacagggcctggcccatgtatggccaggaagtagcacaggctgagtgcaggcccaccc 403271

Qy   2555 tgcttggcccagggggcttcctgaggggagacagagcaacccctggaccccagcctcaaa 2614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403272 tgcttggcccagggggcttcctgaggggagacagagcaacccctggaccccagcctcaaa 403331

Qy   2615 tccaggaccctgccaggcacaggcagggcaggaccagcccacgctgactacagggccacc 2674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403332 tccaggaccctgccaggcacaggcagggcaggaccagcccacgctgactacagggccacc 403391

Qy   2675 ggcaataaaagcccaggagcccatttggagggcctgggcctggctccctcactctcagga 2734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403392 ggcaataaaagcccaggagcccatttggagggcctgggcctggctccctcactctcagga 403451

Qy   2735 aatgctgacccatgggcaggagactgtggagactgctcctgagcccccagcttccagcag 2794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403452 aatgctgacccatgggcaggagactgtggagactgctcctgagcccccagcttccagcag 403511

Qy   2795 gagggacagtctcaccatttccccagggcacgtggttgagtgggggaacgcccacttcc 2854
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403512 gagggacagtctcaccatttccccagggcacgtggttgagtgggggaacgcccacttcc 403571

Qy   2855 ctgggttagactgccagctcttcctagctggagaggagccctgcctctccgcccctgagc 2914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403572 ctgggttagactgccagctcttcctagctggagaggagccctgcctctccgcccctgagc 403631

Qy   2915 ccactgtgcgtggggctcccgcctccaacccctcgcccagtcccagcagccagccaaaca 2974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403632 ccactgtgcgtggggctcccgcctccaacccctcgcccagtcccagcagccagccaaaca 403691

Qy   2975 cacagaaggggactgccacctccccttgccagctgctgagccgcagagaagtgacggttc 3034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403692 cacagaaggggactgccacctccccttgccagctgctgagccgcagagaagtgacggttc 403751

Qy   3035 ctacacaggacaggggttccttctgggcattacatcgcatagaaatcaataatttgtggt 3094
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403752 ctacacaggacaggggttccttctgggcattacatcgcatagaaatcaataatttgtggt 403811

Qy   3095 gatttggatctgtgttttaatgagtttcacagtgtgattttgattattaattgtgcaagc 3154
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 403812 gatttggatctgtgttttaatgagtttcacagtgtgattttgattattaattgtgcaagc 403871

Qy   3155 ttttcctaataaacgtggagaatcaca 3181
          |||||||||||||||||||||||||
Db 403872 ttttcctaataaacgtggagaatcaca 403898


RESULT   9
US-09-758-466-318
; Sequence 318, Application US/09758466
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PM036
;  CURRENT APPLICATION NUMBER: US/09/758,466
;  CURRENT FILING DATE:  2001-01-11
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  NUMBER OF SEQ ID NOS: 814
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 318
;   LENGTH: 1141
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (404)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (1118)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-758-466-318


  Query Match             23.3%;  Score 740;  DB 7;  Length 1141;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  960;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy    953 ccaccctgtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctg 1012
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 ccaccctgtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctg 61

Qy   1013 agaaggacgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgt 1072
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 agaaggacgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgt 121

Qy   1073 ggtgggggggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtggg 1132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 ggtgggggggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtggg 181

Qy   1133 tcgggaagaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccag 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 tcgggaagaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccag 241

Qy   1193 cggggattcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcact 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 cggggattcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcact 301

Qy   1253 tcaaccggcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctg 1312
          |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db    302 tcaaccggcagatcccggcggca-cttcactcattcagaccgcatggaggtgctatgctg 360

Qy   1313 ccgagaaccccgactcctccacctggaagatctacatccggaaggccccccggagccaca 1372
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    361 ccgagaaccccgactcctccacctggaagatctacatccggaangccccccggagccaca 420

Qy   1373 ctctgctgtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttca 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ctctgctgtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaagttca 480

Qy   1433 agctggacaaagacaatggggtgactcctggagagaagatgctcacagtcccccatatca 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 agctggacaaagacaatggggtgactcctggagagaagatgctcacagtcccccatatca 540

Qy   1493 cgtgcgacccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagtt 1552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 cgtgcgacccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagtt 600

Qy   1553 ctgtaaggaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaaca 1612
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ctgtaaggaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaaca 660

Qy   1613 gcttcgccgaggacctggacctggaaggggagactctgctgacacccatcacccacatct 1672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 gcttcgccgaggacctggacctggaaggggagactctgctgacacccatcacccacatct 720

Qy   1673 cacagctgcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttg 1732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 cacagctgcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttg 780

Qy   1733 tggccaagaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagc 1792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 tggccaagaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagc 840

Qy   1793 agtactcgcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctgg 1852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 agtactcgcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctgg 900
```

```
Qy   1853 accagtccattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcg 1912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 accagtccattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcg 960

Qy   1913 gca 1915
          |||
Db    961 gca 963


RESULT 10
US-09-904-809-19624
; Sequence 19624, Application US/09904809
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-757
;  CURRENT APPLICATION NUMBER: US/09/904,809
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/234,611
;  PRIOR FILING DATE: 1999-01-22
;  NUMBER OF SEQ ID NOS: 21025
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19624
;   LENGTH: 469
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(469)
;   OTHER INFORMATION: n = A,T,C or G
US-09-904-809-19624


  Query Match           13.3%;  Score 422;  DB 7;  Length 469;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-199;
  Matches  422;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2213 gatgggcctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggagg 2272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     47 gatgggcctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggagg 106

Qy   2273 ccacctcctaaaaggcccagagagaagagccccactctcagaggccccaataccccatgg 2332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    107 ccacctcctaaaaggcccagagagaagagccccactctcagaggccccaataccccatgg 166

Qy   2333 accatgctgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccg 2392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    167 accatgctgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccg 226

Qy   2393 gtgtgggggccccgtctcaggtctgagttgttaccccaagcgccctggccccccacatggt 2452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    227 gtgtgggggccccgtctcaggtctgagttgttaccccaagcgccctggccccccacatggt 286

Qy   2453 gatgttgacatcactggcatggtggttgggacccagtggcagggcacagggcctggccca 2512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 gatgttgacatcactggcatggtggttgggacccagtggcagggcacagggcctggccca 346

Qy   2513 tgtatggccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggct 2572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    347 tgtatggccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggct 406

Qy   2573 tcctgaggggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggc 2632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    407 tcctgaggggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggc 466

Qy   2633 ac 2634
          ||
Db    467 ac 468


RESULT 11
US-09-909-627-12677
; Sequence 12677, Application US/09909627
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-766
;  CURRENT APPLICATION NUMBER: US/09/909,627
;  CURRENT FILING DATE:  2001-07-19
;  PRIOR APPLICATION NUMBER: 09/277,227
;  PRIOR FILING DATE: 1999-03-23
;  NUMBER OF SEQ ID NOS: 23680
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12677
;   LENGTH: 469
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(469)
;   OTHER INFORMATION: n = A,T,C or G
US-09-909-627-12677


  Query Match           13.3%;  Score 422;  DB 7;  Length 469;
  Best Local Similarity  100.0%;  Pred. No. 8.7e-199;
  Matches  422;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2213 gatgggcctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggagg 2272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     47 gatgggcctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggagg 106

Qy   2273 ccacctcctaaaaggcccagagagaagagccccactctcagaggccccaataccccatgg 2332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    107 ccacctcctaaaaggcccagagagaagagccccactctcagaggccccaataccccatgg 166

Qy   2333 accatgctgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccg 2392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    167 accatgctgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccg 226

Qy   2393 gtgtgggggccccgtctcaggtctgagttgttaccccaagcgccctggccccccacatggt 2452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    227 gtgtgggggccccgtctcaggtctgagttgttaccccaagcgccctggccccccacatggt 286

Qy   2453 gatgttgacatcactggcatggtggttgggacccagtggcagggcacagggcctggccca 2512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 gatgttgacatcactggcatggtggttgggacccagtggcagggcacagggcctggccca 346

Qy   2513 tgtatggccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggct 2572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    347 tgtatggccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggct 406

Qy   2573 tcctgaggggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggc 2632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    407 tcctgaggggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggc 466

Qy   2633 ac 2634
          ||
Db    467 ac 468


RESULT 12
US-60-313-371-1497
; Sequence 1497, Application US/60313371
; GENERAL INFORMATION:
;  APPLICANT: Ring, Huijun Z.
;  APPLICANT:  Malsen, Gareth
;  APPLICANT:  Townley, David
;  APPLICANT:  Morris, MacDonald
;  TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
;  FILE REFERENCE: GX-0013-5 P
;  CURRENT APPLICATION NUMBER: US/60/313,371
;  CURRENT FILING DATE:  2001-08-16
;  NUMBER OF SEQ ID NOS: 2447
```

```
;  SOFTWARE: PERL Program
; SEQ ID NO 1497
;   LENGTH: 471
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GB:AB015148_1
US-60-313-371-1497


  Query Match           12.5%;  Score 398;  DB 10;  Length 471;
  Best Local Similarity   99.8%;  Pred. No. 7.4e-187;
  Matches  448;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    100 tcgccttcgctgcagctcccggtgccgccgctcgggccggccccccggcaggccctcctc 159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 tcgccttcgctgcagctcccggtgccgccgctcgggccggccccccggcaggccctcctc 60

Qy    160 gttatggccgcggcctcctccccgcccagggccgagaggaagcgctggggttggggccgc 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gttatggccgcggcctcctccccgcccagggccgagaggaagcgctggggttggggccgc 120

Qy    220 ctgccaggcgcccggcggggcagcgcgggcctggccaagaagtgccccttctcgctggag 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ctgccaggcgcccggcggggcagcgcgggcctggccaagaagtgccccttctcgctggag 180

Qy    280 ctggcggagggcggcccggcgggcggcgcgctctacgcgcccatcgcgcccggcgcccca 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ctggcggagggcggcccggcgggcggcgcgctctacgcgcccatcgcgcccggcgcccca 240

Qy    340 ggtcccgcgccccctgcgtccccggccgcgcccgccgcgcccccagttgcctccgacctt 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ggtcccgcgccccctgcgtccccggccgcgcccgccgcgcccccagttgcctccgacctt 300

Qy    400 ggcccgcggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccg 459
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    301 ggcccgcggccgccggtgagcctagacccgcgcgtctccatttacagcacgcgccgcccg 360

Qy    460 gtgttggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggc 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 gtgttggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggc 420

Qy    520 tggaaatgcttcgtttaccacttcgccgt 548
          ||||||||||||||||||||||||||||||
Db    421 tggaaatgcttcgtttaccacttcgccgt 449


RESULT  13
US-09-933-524-85039
; Sequence 85039, Application US/09933524
; GENERAL INFORMATION:
;  APPLICANT: Drmanac, Radoje T.
;  APPLICANT:  Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Dickson, Mark
;  APPLICANT:  Jones, Lee W.
;  TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION:  From Various Libraries
;  FILE REFERENCE: 774
;  CURRENT APPLICATION NUMBER: US/09/933,524
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: 09/528,409
;  PRIOR FILING DATE: 2000-03-17
;  NUMBER OF SEQ ID NOS: 116231
;  SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 85039
;   LENGTH: 432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-933-524-85039


  Query Match           10.4%;  Score 332;  DB 9;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-154;
  Matches  332;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1663 acccacatctcacagctgcgggaacaccatcgggccaccattaaggtcattcgacgcatg 1722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 acccacatctcacagctgcgggaacaccatcgggccaccattaaggtcattcgacgcatg 160

Qy   1723 cagtactttgtggccaagaagaaattccagcaagcgcggaagccttacgatgtgcgggac 1782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 cagtactttgtggccaagaagaaattccagcaagcgcggaagccttacgatgtgcgggac 220

Qy   1783 gtcattgagcagtactcgcagggccacctcaacctcatggtgcgcatcaaggagctgcag 1842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 gtcattgagcagtactcgcagggccacctcaacctcatggtgcgcatcaaggagctgcag 280

Qy   1843 aggaggctggaccagtccattgggaagccctcactgttcatctccgtctcagaaaagagc 1902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 aggaggctggaccagtccattgggaagccctcactgttcatctccgtctcagaaaagagc 340

Qy   1903 aaggatcgcggcagcaacacgatcggcgcccgcctgaaccgagtagaagacaaggtgacg 1962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 aaggatcgcggcagcaacacgatcggcgcccgcctgaaccgagtagaagacaaggtgacg 400

Qy   1963 cagctggaccagaggctggcactcatcaccga 1994
          |||||||||||||||||||||||||||||||
Db    401 cagctggaccagaggctggcactcatcaccga 432


RESULT  14
US-09-933-524-18451
; Sequence 18451, Application US/09933524
; GENERAL INFORMATION:
;  APPLICANT: Drmanac, Radoje T.
;  APPLICANT:  Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Dickson, Mark
;  APPLICANT:  Jones, Lee W.
;  TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
;  TITLE OF INVENTION:  From Various Libraries
;  FILE REFERENCE: 774
;  CURRENT APPLICATION NUMBER: US/09/933,524
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: 09/528,409
;  PRIOR FILING DATE: 2000-03-17
;  NUMBER OF SEQ ID NOS: 116231
;  SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 18451
;   LENGTH: 455
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-933-524-18451


  Query Match            9.9%;  Score 316;  DB 9;  Length 455;
  Best Local Similarity   99.7%;  Pred. No. 4.1e-146;
  Matches  366;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1817 tcatggtgcgcatcaaggagctgcagaggaggctggaccagtccattgggaagccctcac 1876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 tcatggtgcgcatcaaggagctgcagaggaggctggaccagtccattgggaagccctcac 128

Qy   1877 tgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacgatcggcgcccgcc 1936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 tgttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacgatcggcgcccgcc 188

Qy   1937 tgaaccgagtagaagacaaggtgacgcagctggaccagaggctggcactcatcaccgaca 1996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 tgaaccgagtagaagacaaggtgacgcacctggaccagaggctggcactcatcaccgaca 248

Qy   1997 tgcttcaccagctgctctccttgcacggtggcagcacccccggcagcggcggccccccca 2056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 tgcttcaccagctgctctccttgcacggtggcagcacccccggcagcggcggccccccca 308
```

```
Qy   2057 gagagggcggggcccacatcacccagccctgcggcagtggcggctccgtcgaccctgagc 2116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 gagagggcggggcccacatcacccagccctgcggcagtggcggctccgtcgaccctgagc 368

Qy   2117 tcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtgcccaggaggggcc 2176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 tcttcctgcccagcaacaccctgcccacctacgagcagctgaccgtgcccaggaggggcc 428

Qy   2177 ccgatga 2183
          |||||||
Db    429 ccgatga 435


RESULT 15
US-09-904-703-5165
; Sequence 5165, Application US/09904703
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-758CON1
;  CURRENT APPLICATION NUMBER: US/09/904,703
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/210,298
;  PRIOR FILING DATE: 1998-12-09
;  NUMBER OF SEQ ID NOS: 17812
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5165
;   LENGTH: 412
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-904-703-5165


  Query Match             9.7%;  Score 307;  DB 7;  Length 412;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-141;
  Matches  407;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   2421 tgttaccccaagcgccctggcccccacatggtgatgttgacatcactggcatggtggttg 2480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 tgttaccccaagcgccctggcccccacatggtgatgttgacatcactggcatggtggttg 63

Qy   2481 ggacccagtggcagggcacagggcctggcccatgtatggccaggaagtagcacaggctga 2540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 ggacccagtggcagggcacagggcctggcccatgtatggccaggaagtagcacaggctga 123

Qy   2541 gtgcaggcccaccctgcttggcccaggggctcctgaggggagacagagcaacccctgg 2600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 gtgcaggcccaccctgcttggcccaggggctcctgaggggagacagagcaacccctgg 183

Qy   2601 accccagcctcaaatccaggaccctgccaggcacaggcagggcaggaccagcccacgctg 2660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    184 accccagcctcaaatccaggaccctgccaggcacaggcagggcaggaccagcccacgctg 243

Qy   2661 actacagggccaccggcaataaaagcccaggagcccatttggagggcctgggcctggctc 2720
          |||||||||||| |||||||||||||||| |||||||||||||||||||||||||||||||
Db    244 actacagggccgccggcaataaaagcccaagagcccatttggagggcctgggcctggctc 303

Qy   2721 cctcactctcaggaaatgctgacccatgggcaggagactgtggagactgctcctgagccc 2780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 cctcactctcaggaaatgctgacccatgggcaggagactgtggagactgctcctgagccc 363

Qy   2781 ccagcttccagcaggagggacagtctcaccatttccccagggcacgtgg 2829
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 ccagcttccagcaggagggacagtctcaccatttccccagggcacgtgg 412


Search completed: November  2, 2001, 15:05:20
Job time: 6746 sec
```

GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 12:09:44 ; Search time 1660.94 Seconds
(without alignments)
18103.921 Million cell updates/sec

Title: US-09-135-010A-1
Perfect score: 3181
Sequence: 1 ctgccccctccggccccgcc.....aataaacgtggagaatcaca 3181

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 12

Total number of hits satisfying chosen parameters: 2312605

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
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3: gb_est3:*
4: gb_est4:*
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7: gb_est7:*
8: gb_est8:*
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254: em_gss_rod7:*
255: em_gss_rod8:*
256: gb_gss35:*
257: gb_gss36:*
258: gb_gss37:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| c 1 | 727 | 22.9 | 851 | 106 | AL577771 | AL577771 AL577771 |
| 2 | 529 | 16.6 | 679 | 138 | BE675840 | BE675840 7f17a09.x |
| 3 | 514 | 16.2 | 600 | 108 | AU141948 | AU141948 AU141948 |
| 4 | 511 | 16.1 | 943 | 106 | AL577772 | AL577772 AL577772 |
| 5 | 507 | 15.9 | 812 | 152 | BG328061 | BG328061 602427108 |
| 6 | 497 | 15.6 | 775 | 153 | BG385872 | BG385872 602454417 |
| c 7 | 491 | 15.4 | 491 | 110 | AW006385 | AW006385 wt04g12.x |
| c 8 | 474 | 14.9 | 488 | 113 | AW205864 | AW205864 UI-H-BI1- |
| 9 | 461 | 14.5 | 461 | 19 | AI347525 | AI347525 qo98e02.x |
| 10 | 442 | 13.9 | 442 | 24 | AI769029 | AI769029 wg31h01.x |
| c 11 | 441 | 13.9 | 494 | 112 | AW192638 | AW192638 xl48b04.x |
| 12 | 440 | 13.8 | 493 | 20 | AI439544 | AI439544 tc90b05.x |
| c 13 | 408 | 12.8 | 484 | 110 | AW005483 | AW005483 ws94f02.x |
| 14 | 393 | 12.4 | 451 | 144 | BF109081 | BF109081 7150b06.x |
| 15 | 387 | 12.2 | 418 | 19 | AI344361 | AI344361 qp07e12.x |
| 16 | 378 | 11.9 | 684 | 155 | BG548631 | BG548631 602576435 |
| 17 | 367 | 11.5 | 535 | 169 | BF798694 | BF798694 RC1-CI011 |
| c 18 | 363 | 11.4 | 481 | 24 | AI738525 | AI738525 wi33a11.x |
| c 19 | 363 | 11.4 | 556 | 108 | AU159371 | AU159371 AU159371 |
| c 20 | 346 | 10.9 | 683 | 19 | AI344314 | AI344314 tc03e03.x |
| c 21 | 333 | 10.5 | 631 | 164 | BE159001 | BE159001 MR0-HT040 |
| 22 | 318 | 10.0 | 490 | 24 | AI739442 | AI739442 wi13e04.x |
| c 23 | 313 | 9.8 | 328 | 102 | AI826701 | AI826701 wk46e04.x |
| c 24 | 305 | 9.6 | 318 | 112 | AW136422 | AW136422 UI-H-BI1- |
| c 25 | 269 | 8.5 | 371 | 121 | AW866858 | AW866858 CM3-SN003 |
| c 26 | 255 | 8.0 | 460 | 165 | BE222815 | BE222815 hu53g08.x |
| c 27 | 253 | 8.0 | 253 | 19 | AI344116 | AI344116 tc02b06.x |
| c 28 | 251 | 7.9 | 339 | 9 | AA603649 | AA603649 np20g12.s |
| c 29 | 251 | 7.9 | 476 | 12 | AA824263 | AA824263 aj29e05.s |
| 30 | 242 | 7.6 | 565 | 191 | W93500 | W93500 zd96e05.s1 |
| c 31 | 233 | 7.3 | 244 | 169 | BF755715 | BF755715 PM4-CT056 |
| c 32 | 232 | 7.3 | 233 | 111 | AW057846 | AW057846 wv90a10.x |
| c 33 | 213 | 6.7 | 377 | 103 | AI869254 | AI869254 wl51e10.x |
| 34 | 206 | 6.5 | 323 | 19 | AI344946 | AI344946 tb01c01.x |
| 35 | 206 | 6.5 | 437 | 19 | AI344925 | AI344925 tb01a01.x |
| 36 | 206 | 6.5 | 442 | 19 | AI344927 | AI344927 tb01a03.x |
| 37 | 205 | 6.4 | 258 | 19 | AI345107 | AI345107 ta95e07.x |
| c 38 | 205 | 6.4 | 391 | 20 | AI473902 | AI473902 ti68c11.x |
| c 39 | 205 | 6.4 | 1003 | 138 | BE617784 | BE617784 601441990 |
| 40 | 202 | 6.4 | 449 | 122 | AW953589 | AW953589 EST365659 |
| c 41 | 200 | 6.3 | 405 | 123 | AW978648 | AW978648 EST390757 |
| 42 | 197 | 6.2 | 197 | 112 | AW138991 | AW138991 UI-H-BI1- |
| 43 | 197 | 6.2 | 309 | 6 | AA352245 | AA352245 EST60369 |
| 44 | 196 | 6.2 | 465 | 122 | AW949927 | AW949927 EST361997 |
| 45 | 184 | 5.8 | 270 | 113 | AW268275 | AW268275 xr95a03.x |

ALIGNMENTS

RESULT 1
AL577771/c
LOCUS AL577771 851 bp mRNA EST 16-FEB-2001
DEFINITION AL577771 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK007YA04 3 prime, mRNA sequence.
ACCESSION AL577771
VERSION AL577771.1 GI:12941220
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 851)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .851
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DK007YA04"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 154 a 249 c 273 g 173 t 2 others
ORIGIN

Query Match 22.9%; Score 727; DB 106; Length 851;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 827; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   2289 ccagagagaagagccccactctcagaggccccaataccccatggaccatgctgtctggca 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    841 CCAGAGAGAAGAGCCCCACTCTCAGAGGCCCCAATACCCCATGGACCATGCTGTCTGGMA 782

Qy   2349 cagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggggccccgtc 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CAGCCTGCACTTGGGGGCTCAGCAAGGCCACCTCTTCCTGGCCGGTGTGGGGGCCCCGTC 722

Qy   2409 tcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttgacatcactg 2468
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Db    721 TCAGGTCTGAGTTGTTACCCCAAGCGCCCTGGCCCCCACATGGTGATGTTGACATCACTG 662

Qy   2469 gcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggccaggaagt 2528
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Db    661 GCATGGTGGTTGGGACCCAGTGGCAGGGCACAGGGCCTGGCCCATGTATGGCCAGGAAGT 602

Qy   2529 agcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgaggggagacag 2588
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Db    601 AGCACAGGCTGAGTGCAGGCCCACCCTGCTTGGCCCAGGGGGCTTCCTGAGGGGAGACAG 542

Qy   2589 agcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcagggcaggac 2648
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Db    541 AGCAACCCCTGGACCCCAGCCTCAAATCCAGGACCCTGCCAGGCACAGGCAGGGCAGGAC 482

Qy   2649 cagcccacgctgactacagggccaccggcaataaaagcccaggagcccatttggagggcc 2708
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Db    481 CAGCCCACGCTGACTACAGGGCCGCCGGCAATAAAAGCCCAGGAGCCCATTTGGAGGGCC 422

Qy   2709 tgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactgtggagact 2768
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Db    421 TGGGCCTGGCTCCCTCACTCTCAGGAAATGCTGACCCATGGGCAGGAGACTGTGGAGACT 362

Qy   2769 gctcctgagcccccagcttccagcaggagggacagtctcaccatttccccagggcacgtg 2828
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCTCCTGAGCCCCCAGCTTCCAGCAGGAGGGACAGTCTCACCATTTCCCCAGGGCACGTG 302

Qy   2829 gttgagtgggggggaacgcccacttccctgggttagactgccagctcttcctagctggaga 2888
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Db    301 GTTGAGTGGGGGGAACGCCCACTTCCCTGGGTTAGACTGCCAGCTCTTCCTAGCTGGAGA 242

Qy   2889 ggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctccaacccctc 2948
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Db    241 GGAGCCCTGCCTCTCCGCCCCTGAGCCCACTGTGCGTGGGGCTCCCGCCTCCAACCCCTC 182

Qy   2949 gcccagtcccagcagccagccaaacacacagaaggggactgccacctccccttgccagct 3008
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3009 gctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgggcattaca 3068
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTGAGCCGCAGAGAAGTGACGGTTCCTACACAGGACAGGGGTTCCTTCTGGGCATTACA 62

Qy   3069 tcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatga 3117
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGCATAGAAATCAATAATTTGTGGTGATTTGGATCTGTGTTTTAATGA 13


RESULT   2
BE675840
LOCUS       BE675840      679 bp    mRNA            EST       08-SEP-2000
DEFINITION  7f17a09.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294904 3'
            similar to TR:O60607 O60607 SLOW DELAYED RECTIFIER CHANNEL SUBUNIT.
            ;contains PTR5.t3 TAR1 repetitive element ;, mRNA sequence.
ACCESSION   BE675840
VERSION     BE675840.1  GI:10036381
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 465.
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                     /clone_lib="NCI_CGAP_CLL1"
                     /tissue_type="B-cell, chronic lymphotic leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       93 a    224 c    207 g    155 t
ORIGIN


  Query Match           16.6%;  Score 529;  DB 138;  Length 679;
  Best Local Similarity  99.7%;  Pred. No. 2.2e-254;
  Matches  629;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    405 gcggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccggtgtt 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTT 60

Qy    465 ggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggctggaa 524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCCTCGAGCGTCCCACCGGCTGGAA 120

Qy    525 atgcttcgtttaccacttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgt 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATGCTTCGTTTACCACTTCGCCGTCTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGT 180

Qy    585 gctgtccaccatcgagcagtatgccgccctggccacggggactctcttctggatggagat 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCTGTCCACCATCGAGCAGTATGCCGCCCTGGCCACGGGGACTCTCTTCTGGATGGAGAT 240

Qy    645 cgtgctggtggtgttcttcgggacggagtacgtggtccgcctctggtccgccggctgccg 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGTGCTGGTGGTGTTCTTCGGGACGGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCG 300

Qy    705 cagcaagtacgtgggcctctgggggcggctgcgctttgcccggaagcccatttccatcat 764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGCAAGTACGTGGGCCTCTGGGGGCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCAT 360

Qy    765 cgacctcatcgtggtcgtggcctccatggtggtcctctgcgtgggctccaaggggcaggt 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CGACCTCATCGTGGTCGTGGCCTCCATGGTGGTCCTCTGCGTGGGCTCCAAGGGGCAGGT 420

Qy    825 gtttgccacgtcggccatcaggggcatccgcttcctgcagatcctgaggatgctacacgt 884
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTTGCCACGTCGGCCATCAGGGGCATCCGCTTCCTGCAGATCCTGAGGATGCTACACGT 480

Qy    885 cgaccgccagggaggcacctggaggctcctgggctccgtggtcttcatccaccgccagga 944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CGACCGCCATGGAGGCACCTGGAGGCTCCTGTGCTCCGTGGTCTTCATCCACCGCCAGGA 540

Qy    945 gctgataaccaccctgtacatcggcttcctgggcctcatcttctcctcgtactttgtgta 1004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCTGATAACCACCCTGTACATCGGCTTCCTGGGCCTCATCTTCTCCTCGTACTTTGTGTA 600

Qy   1005 cctggctgagaaggacgcggtgaacgagtca 1035
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Db    601 CCTGGCTGAGAAGGACGCGGTGAACGAGTCA 631


RESULT   3
AU141948
LOCUS       AU141948      600 bp    mRNA            EST       25-OCT-2000
DEFINITION  AU141948 THYRO1 Homo sapiens cDNA clone THYRO1001510 5', mRNA
            sequence.
ACCESSION   AU141948
VERSION     AU141948.1  GI:11003469
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 600)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
     source          1. .600
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="THYRO1001510"
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                     /clone_lib="THYRO1"
                     /tissue_type="thyroid gland"
                     /note="Vector: pME18SFL3"
BASE COUNT       86 a    183 c    193 g    134 t      4 others
ORIGIN


  Query Match             16.2%;  Score 514;  DB 108;  Length 600;
  Best Local Similarity   99.8%;  Pred. No. 7.6e-247;
  Matches  564;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     560 tcctggtctgcctcatcttcagcgtgctgtccaccatcgagcagtatgccgccctggcca 619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TCCTGGTCTGCCTCATCTTCAGCGTGCTGTCCACCATCGAGCAGTATGCCGCCCTGGCCA 60

Qy     620 cggggactctcttctggatggagatcgtgctggtggtgttcttcgggacggagtacgtgg 679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGGGGACTCTCTTCTGGATGGAGATCGTGCTGGTGGTGTTCTTCGGGACGGAGTACGTGG 120

Qy     680 tccgcctctggtccgccggctgccgcagcaagtacgtgggcctctgggggcggctgcgct 739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TCCGCCTCTGGTCCGCCGGCTGCCGCAGCAAGTACGTGGGCCTCTGGGGGCGGCTGCGCT 180

Qy     740 ttgcccggaagcccatttccatcatcgacctcatcgtggtcgtggcctccatggtggtcc 799
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TTGCCCGGAAGCCCATTTCCATCATCGACCTCATCGTGGTCGTGGCCTCCATGGTGGTCC 240

Qy     800 tctgcgtgggctccaaggggcaggtgtttgccacgtcggccatcaggggcatccgcttcc 859
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCTGCGTGGGCTCCAAGGGGCAGGTGTTTGCCACGTCGGCCATCAGGGGCATCCGCTTCC 300

Qy     860 tgcagatcctgaggatgctacacgtcgaccgccagggaggcacctggaggctcctgggct 919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGCAGATCCTGAGGATGCTACACGTCGACCGCCAGGGAGGCACCTGGAGGCTCCTGGGCT 360

Qy     920 ccgtggtcttcatccaccgccaggagctgataaccaccctgtacatcggcttcctgggcc 979
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Db     361 CCGTGGTCTTCATCCACCGNCAGGAGCTGATAACCACCCTGTACATCGGCTTCCTGGGCC 420

Qy     980 tcatcttctcctcgtactttgtgtacctggctgagaaggacgcggtgaacgagtcaggcc 1039
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TCATCTTCTCCTCGTACTTTGTGTACCTGGCTGAGAAGGACGCGGTGAACGAGTCAGGCC 480

Qy    1040 gcgtggagttcggcagctacgcagatgcgctgtggtgggggtggtcacagtcaccacca 1099
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GCGTGGAGTTCGGCAGCTACGCAGATGCGCTGTGGTGGGGGGTGGTCACAGTCACCACCA 540

Qy    1100 tcggctatggggacaaggtgcccca 1124
           |||||||||||||||||||||||||
Db     541 TCGGCTATGGGGACAAGGTGCCCCA 565


RESULT   4
AL577772
LOCUS       AL577772      943 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL577772 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DK007YA04 5
            prime, mRNA sequence.
ACCESSION   AL577772
VERSION     AL577772.1  GI:12941222
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 943)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .943
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DK007YA04"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      181 a    296 c    319 g    144 t      3 others
ORIGIN


  Query Match             16.1%;  Score 511;  DB 106;  Length 943;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-245;
  Matches  511;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1894 gaaaagagcaaggatcgcggcagcaacacgatcggcgcccgcctgaaccgagtagaagac 1953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     269 GAAAAGAGCAAGGATCGCGGCAGCAACACGATCGGCGCCCGCCTGAACCGAGTAGAAGAC 328

Qy    1954 aaggtgacgcagctggaccagaggctggcactcatcaccgacatgcttcaccagctgctc 2013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     329 AAGGTGACGCAGCTGGACCAGAGGCTGGCACTCATCACCGACATGCTTCACCAGCTGCTC 388

Qy    2014 tccttgcacggtggcagcacccccggcagcggcggccccccccagagagggcggggcccac 2073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     389 TCCTTGCACGGTGGCAGCACCCCCGGCAGCGGCGGCCCCCCCAGAGAGGGCGGGGCCCAC 448

Qy    2074 atcacccagccctgcggcagtggcggctccgtcgaccctgagctcttcctgcccagcaac 2133
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     449 ATCACCCAGCCCTGCGGCAGTGGCGGCTCCGTCGACCCTGAGCTCTTCCTGCCCAGCAAC 508

Qy    2134 accctgcccacctacgagcagctgaccgtgcccaggaggggccccgatgaggggtcctga 2193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     509 ACCCTGCCCACCTACGAGCAGCTGACCGTGCCCAGGAGGGGCCCCGATGAGGGGTCCTGA 568

Qy    2194 ggaggggatggggctgggggatgggcctgagtgagaggggaggccaagagtggccccacc 2253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 GGAGGGGATGGGGCTGGGGGATGGGCCTGAGTGAGAGGGGAGGCCAAGAGTGGCCCCACC 628

Qy    2254 tggccctctctgaaggaggccacctcctaaaaggcccagagagaagagccccactctcag 2313
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Db     629 TGGCCCTCTCTGAAGGAGGCCACCTCCTAAAAGGCCCAGAGAGAAGAGCCCCACTCTCAG 688

Qy    2314 aggccccaataccccatggaccatgctgtctggcacagcctgcacttgggggctcagcaa 2373
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     689 AGGCCCCAATACCCCATGGACCATGCTGTCTGGCACAGCCTGCACTTGGGGGCTCAGCAA 748

Qy    2374 ggccacctcttcctggccggtgtgggggccc 2404
           ||||||||||||||||||||||||||||||||
Db     749 GGCCACCTCTTCCTGGCCGGTGTGGGGGCCC 779


RESULT   5
BG328061
LOCUS       BG328061      812 bp    mRNA            EST       27-FEB-2001
DEFINITION  602427108F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4546777 5',
            mRNA sequence.
ACCESSION   BG328061
VERSION     BG328061.1  GI:13134499
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1233  row: o  column: 02
            High quality sequence stop: 725.
FEATURES             Location/Qualifiers
     source          1. .812
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4546777"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      193 a    234 c    233 g    152 t
ORIGIN


  Query Match             15.9%;  Score 507;  DB 152;  Length 812;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-243;
  Matches  507;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    998 ttgtgtacctggctgagaaggacgcggtgaacgagtcaggccgcgtggagttcggcagct 1057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     18 TTGTGTACCTGGCTGAGAAGGACGCGGTGAACGAGTCAGGCCGCGTGGAGTTCGGCAGCT 77

Qy   1058 acgcagatgcgctgtggtgggggtggtcacagtcaccaccatcggctatggggacaagg 1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 ACGCAGATGCGCTGTGGTGGGGGGTGGTCACAGTCACCACCATCGGCTATGGGGACAAGG 137

Qy   1118 tgccccagacgtgggtcgggaagaccatcgcctcctgcttctctgtctttgccatctcct 1177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 TGCCCCAGACGTGGGTCGGGAAGACCATCGCCTCCTGCTTCTCTGTCTTTGCCATCTCCT 197

Qy   1178 tctttgcgctcccagcggggattcttggctcggggtttgccctgaaggtgcagcagaagc 1237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 TCTTTGCGCTCCCAGCGGGGATTCTTGGCTCGGGGTTTGCCCTGAAGGTGCAGCAGAAGC 257

Qy   1238 agaggcagaagcacttcaaccggcagatcccggcggcagcctcactcattcagaccgcat 1297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 AGAGGCAGAAGCACTTCAACCGGCAGATCCCGGCGGCAGCCTCACTCATTCAGACCGCAT 317

Qy   1298 ggaggtgctatgctgccgagaaccccgactcctccacctggaagatctacatccggaagg 1357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 GGAGGTGCTATGCTGCCGAGAACCCCGACTCCTCCACCTGGAAGATCTACATCCGGAAGG 377

Qy   1358 ccccccggagccacactctgctgtcacccagccccaaacccaagaagtctgtggtggtaa 1417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378 CCCCCCGGAGCCACACTCTGCTGTCACCCAGCCCCAAACCCAAGAAGTCTGTGGTGGTAA 437

Qy   1418 agaaaaaaaagttcaagctggacaaagacaatggggtgactcctggagagaagatgctca 1477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438 AGAAAAAAAAGTTCAAGCTGGACAAAGACAATGGGGTGACTCCTGGAGAGAAGATGCTCA 497

Qy   1478 cagtcccccatatcacgtgcgaccccc 1504
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Db    498 CAGTCCCCCATATCACGTGCGACCCCC 524


RESULT   6
BG385872
LOCUS       BG385872      775 bp    mRNA            EST       12-MAR-2001
DEFINITION  602454417F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4582565 5',
            mRNA sequence.
ACCESSION   BG385872
VERSION     BG385872.1  GI:13279276
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 775)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: NIH Intramural Sequencing Center
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1305  row: b  column: 06
            High quality sequence stop: 772.
FEATURES             Location/Qualifiers
     source          1. .775
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4582565"
                     /clone_lib="NIH_MGC_15"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT      157 a    258 c    237 g    123 t
ORIGIN


  Query Match             15.6%;  Score 497;  DB 153;  Length 775;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-238;
  Matches  617;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy   2224 gtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctcctaa 2283
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GTGAGAGGGGAGGCCAAGAGTGGCCCCACCTGGCCCTCTCTGAAGGAGGCCACCTCCTAA 61

Qy   2284 aaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgctgtc 2343
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Db     62 AAGGCCCAGAGAGAAGAGCCCCACTCTCAGAGGCCCCAATACCCCATGGACCATGCTGTC 121

Qy   2344 tggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggggcc 2403
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Db    122 TGGCACAGCCTGCACTTGGGGGCTCAGCAAGGCCACCTCTTCCTGGCCGGTGTGGGGGCC 181

Qy   2404 ccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttgacat 2463
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Db    182 CCGTCTCAGGTCTGAGTTGTTACCCCAAGCGCCCTGGCCCCCACATGGTGATGTTGACAT 241

Qy   2464 cactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggccag 2523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 CACTGGCATGGTGGTTGGGACCCAGTGGCAGGGCACAGGGCCTGGCCCATGTATGGCCAG 301
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Qy   2524 gaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggcttcctgagggga 2583
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Db    302 GAAGTAGCACAGGCTGAGTGCAGGCCCACCCTGCTTGGCCCA-GGGGCTTCCTGAGGGGA 360

Qy   2584 gacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcagggc 2643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACAGAGCAACCCCTGGACCCCAGCCTCAAATCCAGGACCCTGCCAGGCACAGGCAGGGC 420

Qy   2644 aggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatttgga 2703
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGACCAGCCCACGCTGACTACAGGGCCACCGGCAATAAAAGCCCAGGAGCCCATTTGGA 480

Qy   2704 gggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactgtgg 2763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGGCCTGGGCCTGGCTCCCTCACTCTCAGGAAATGCTGACCCATGGGCAGGAGACTGTGG 540

Qy   2764 agactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccagggc 2823
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Db    541 AGACTGCTCCTGAGCCCCCAGCTTCCAGCAGGAGGGACAGTCTCACCATTTCCCCAGGGC 600

Qy   2824 acgtggttgagtgggggg 2841
          ||||||||||||||||||
Db    601 ACGTGGTTGAGTGGGGGG 618


RESULT   7
AW006385/c
LOCUS       AW006385      491 bp    mRNA            EST       08-MAR-2000
DEFINITION  wt04g12.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2506534 3'
            similar to contains PTR5.b2 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AW006385
VERSION     AW006385.1  GI:5855163
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
            , Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arraying: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 686   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 455.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2506534"
                     /clone_lib="NCI_CGAP_Co3"
                     /sex="pooled"
                     /tissue_type="colon"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from 12 pooled bulk tumor samples and primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library went through one round of
                     normalization. "
BASE COUNT      111 a    133 c    145 g    102 t
ORIGIN


  Query Match             15.4%;  Score 491;  DB 110;  Length 491;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-235;
  Matches  491;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2690 ggagcccatttggagggcctgggcctggctccctcactctcaggaaatgctgacccatgg 2749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    491 GGAGCCCATTTGGAGGGCCTGGGCCTGGCTCCCTCACTCTCAGGAAATGCTGACCCATGG 432

Qy   2750 gcaggagactgtggagactgctcctgagcccccagcttccagcaggagggacagtctcac 2809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    431 GCAGGAGACTGTGGAGACTGCTCCTGAGCCCCCAGCTTCCAGCAGGAGGGACAGTCTCAC 372

Qy   2810 catttccccagggcacgtggttgagtgggggaacgcccacttccctgggttagactgcc 2869
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    371 CATTTCCCCAGGGCACGTGGTTGAGTGGGGGGAACGCCCACTTCCCTGGGTTAGACTGCC 312

Qy   2870 agctcttcctagctggagaggagccctgcctctccgcccctgagcccactgtgcgtgggg 2929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    311 AGCTCTTCCTAGCTGGAGAGGAGCCCTGCCTCTCCGCCCCTGAGCCCACTGTGCGTGGGG 252

Qy   2930 ctcccgcctccaacccctcgcccagtcccagcagccagccaaacacacagaaggggactg 2989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 CTCCCGCCTCCAACCCCTCGCCCAGTCCCAGCAGCCAGCCAAACACACAGAAGGGGACTG 192

Qy   2990 ccacctcccccttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggg 3049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    191 CCACCTCCCCTTGCCAGCTGCTGAGCCGCAGAGAAGTGACGGTTCCTACACAGGACAGGG 132

Qy   3050 gttccttctgggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgt 3109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    131 GTTCCTTCTGGGCATTACATCGCATAGAAATCAATAATTTGTGGTGATTTGGATCTGTGT 72

Qy   3110 tttaatgagtttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacg 3169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     71 TTTAATGAGTTTCACAGTGTGATTTTGATTATTAATTGTGCAAGCTTTTCCTAATAAACG 12

Qy   3170 tggagaatcac 3180
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Db     11 TGGAGAATCAC 1


RESULT   8
AW205864/c
LOCUS       AW205864      488 bp    mRNA            EST       02-DEC-1999
DEFINITION  UI-H-BI1-afv-c-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
            IMAGE:2722967 3', mRNA sequence.
ACCESSION   AW205864
VERSION     AW205864.1  GI:6505268
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward
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           POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2722967"
                     /clone_lib="NCI_CGAP_Sub3"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NCI_CGAP_Sub3 library is a subtracted library derived from
                     the  NCI_CGAP_Sub1 library, which is a subtracted library
                     derived from BI.  BI constitutes a mixture of 21
                     normalized or subtracted NCI_CGAP  libraries: NCI_CGAP_Co4
                     , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
                     NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
                     NCI_CGAP_Kid3,  NCI_CGAP_Kid11, NCI_CGAP_Lym2,
                     NCI_CGAP_Br2, NCI_CGAP_Co8,  NCI_CGAP_CLL1, NCI_CGAP_Lei2,
                     NCI_CGAP_Brn23, NCI_CGAP_Lu5,  NCI_CGAP_Lu24,
                     NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
                     NCI_CGAP_Brn25.  These 21 libraries were pooled and a
                     single-stranded DNA  preparation of the resulting mixture
                     was used as a tracer in a subtractive  hybridization with
                     a driver whose composition is detailed below:
                     NCI_CGAP_Kid3 pool 1    LLAM 3334-3337, 3682-3683,
                     3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
                     , 1500552-1502855); NCI_CGAP_Kid5 pool 1    LLAM 3338-3342
                     , 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
                     1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
                     LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
                     1520904-1522439); NCI_CGAP_GC4 pool 1    LLAM 3164-3167,
                     3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
                     1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
                     LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
                     985608-986759, 1101192-1101959, 1217928-1220615);
                     NCI_CGAP_Co10 pool 1    LLAM 2644-2653, 2871-2872 (IMAGE
                     CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
                     was performed as previously described [Bonaldo, Lennon &
                     Soares (1996): Normalization and Subtraction: Two
                     Approaches To  Facilitate Gene Discovery. Genome Research
                     6, 791-806.
                     TAG_LIB=NCI_CGAP_Kid3
                     TAG_TISSUE=kidney
                     TAG_SEQ=AATGC"
BASE COUNT      108 a    125 c    141 g    114 t
ORIGIN


  Query Match             14.9%;  Score 474;  DB 113;  Length 488;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-227;
  Matches  474;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2708 ctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactgtggagac 2767
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 CTGGGCCTGGCTCCCTCACTCTCAGGAAATGCTGACCCATGGGCAGGAGACTGTGGAGAC 429

Qy   2768 tgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccagggcacgt 2827
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 TGCTCCTGAGCCCCCAGCTTCCAGCAGGAGGGACAGTCTCACCATTTCCCCAGGGCACGT 369

Qy   2828 ggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcctagctggag 2887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 GGTTGAGTGGGGGGAACGCCCACTTCCCTGGGTTAGACTGCCAGCTCTTCCTAGCTGGAG 309

Qy   2888 aggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctccaacccct 2947
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    308 AGGAGCCCTGCCTCTCCGCCCCTGAGCCCACTGTGCGTGGGGCTCCCGCCTCCAACCCCT 249

Qy   2948 cgcccagtcccagcagccagccaaacacacagaaggggactgccacctccccttgccagc 3007
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    248 CGCCCAGTCCCAGCAGCCAGCCAAACACACAGAAGGGGACTGCCACCTCCCCTTGCCAGC 189

Qy   3008 tgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgggcattac 3067
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    188 TGCTGAGCCGCAGAGAAGTGACGGTTCCTACACAGGACAGGGGTTCCTTCTGGGCATTAC 129

Qy   3068 atcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagtttcacagt 3127
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    128 ATCGCATAGAAATCAATAATTTGTGGTGATTTGGATCTGTGTTTTAATGAGTTTCACAGT 69

Qy   3128 gtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatcaca 3181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     68 GTGATTTTGATTATTAATTGTGCAAGCTTTTCCTAATAAACGTGGAGAATCACA 15


RESULT   9
AI347525
LOCUS       AI347525      461 bp    mRNA            EST       02-FEB-1999
DEFINITION  qo98e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916570 3'
            similar to TR:P97414 P97414 POTASSIUM CHANNEL SUBUNIT. ;, mRNA
            sequence.
ACCESSION   AI347525
VERSION     AI347525.1  GI:4084731
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 781   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 402.
FEATURES             Location/Qualifiers
     source          1. .461
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1916570"
                     /clone_lib="NCI_CGAP_Kid5"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT       59 a    158 c    138 g    106 t
ORIGIN


  Query Match             14.5%;  Score 461;  DB 19;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-220;
  Matches  461;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    431 gcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtccagggccgcg 490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGTCTCCATCTACAGCACGCGCCGCCCGGTGTTGGCGCGCACCCACGTCCAGGGCCGCG 60

Qy    491 tctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccacttcgccgtct 550
```

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTACAACTTCCTCGAGCGTCCCACCGGCTGGAAATGCTTCGTTTACCACTTCGCCGTCT 120

Qy    551 tcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagcagtatgccg 610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGTGCTGTCCACCATCGAGCAGTATGCCG 180

Qy    611 ccctggccacggggactctcttctggatggagatcgtgctggtggtgttcttcgggacgg 670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCTGGCCACGGGGACTCTCTTCTGGATGGAGATCGTGCTGGTGGTGTTCTTCGGGACGG 240

Qy    671 agtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcctctgggggc 730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCGCAGCAAGTACGTGGGCCTCTGGGGGC 300

Qy    731 ggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgtggcctcca 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCTGCGCTTTGCCCGGAAGCCCATTTCCATCATCGACCTCATCGTGGTCGTGGCCTCCA 360

Qy    791 tggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggccatcagggca 850
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Db    361 TGGTGGTCCTCTGCGTGGGCTCCAAGGGGCAGGTGTTTGCCACGTCGGCCATCAGGGGCA 420

Qy    851 tccgcttcctgcagatcctgaggatgctacacgtcgaccgc 891
          |||||||||||||||||||||||||||||||||||||||||
Db    421 TCCGCTTCCTGCAGATCCTGAGGATGCTACACGTCGACCGC 461


RESULT 10
AI769029
LOCUS       AI769029      442 bp    mRNA            EST       19-DEC-1999
DEFINITION  wg31h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:2366737 3' similar to TR:O00347 O00347 KIDNEY AND CARDIAC
            VOLTAGE DEPENDENT K+ CHANNEL ;, mRNA sequence.
ACCESSION   AI769029
VERSION     AI769029.1  GI:5235538
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 499   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 426.
FEATURES             Location/Qualifiers
     source          1. .442
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2366737"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     150407, 151176-152327 Soares Nb2HF8-9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                     pool 1:  723720-726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
BASE COUNT       54 a    153 c    136 g     99 t
ORIGIN


  Query Match             13.9%;  Score 442;  DB 24;  Length 442;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-210;
  Matches  442;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    405 gcggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccggtgtt 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTT 60

Qy    465 ggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggctggaa 524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCCTCGAGCGTCCCACCGGCTGGAA 120

Qy    525 atgcttcgtttaccacttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgt 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATGCTTCGTTTACCACTTCGCCGTCTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGT 180

Qy    585 gctgtccaccatcgagcagtatgccgccctggccacggggactctcttctggatggagat 644
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Db    181 GCTGTCCACCATCGAGCAGTATGCCGCCCTGGCCACGGGGACTCTCTTCTGGATGGAGAT 240

Qy    645 cgtgctggtggtgttcttcgggacggagtacgtggtccgcctctggtccgccggctgccg 704
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Db    241 CGTGCTGGTGGTGTTCTTCGGGACGGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCG 300

Qy    705 cagcaagtacgtgggcctctgggggcggctgcgctttgcccggaagcccatttccatcat 764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGCAAGTACGTGGGCCTCTGGGGGCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCAT 360

Qy    765 cgacctcatcgtggtcgtggcctccatggtggtcctctgcgtgggctccaaggggcaggt 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CGACCTCATCGTGGTCGTGGCCTCCATGGTGGTCCTCTGCGTGGGCTCCAAGGGGCAGGT 420

Qy    825 gtttgccacgtcggccatcagg 846
          |||||||||||||||||||||||
Db    421 GTTTGCCACGTCGGCCATCAGG 442


RESULT 11
AW192638/c
LOCUS       AW192638      494 bp    mRNA            EST       29-NOV-1999
DEFINITION  xl48b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2677903 3',
            mRNA sequence.
ACCESSION   AW192638
VERSION     AW192638.1  GI:6471337
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Possible reversed clone: polyT not found
            Seq primer: -40UP from Gibco
            High quality sequence stop: 411.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2677903"
                     /clone_lib="NCI_CGAP_Pan1"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
BASE COUNT      111 a    133 c    144 g    105 t      1 others
ORIGIN

  Query Match             13.9%;  Score 441;  DB 112;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-210;
  Matches  491;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    2690 ggagcccatttggagggcctgggcctggctccctcactctcaggaaatgctgacccatgg 2749
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     494 GGAGCCCATTTGGAGGGCCTGGGCCTGGCTCCCTCACTCTCAGGAAATGCTGACCCATGG 435

Qy    2750 gcaggagactgtggagactgctcctgagcccccagcttccagcaggagggacagtctcac 2809
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     434 GCAGGAGACTGTGGAGACTGCTCCTGAGCCCCCAGCTTCCAGCAGGAGGGACAGTCTCAC 375

Qy    2810 catttccccagggcacgtggttgagtgggggggaacgcccacttccctgggttagactgcc 2869
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     374 CATTTCCNCAGGGCACGTGGTTGAGTGGGGGGAACGCCCACTTCCCTGGGTTAGACTGCC 315

Qy    2870 agctcttcctagctggagaggagccctgcctctccgcccctgagcccactgtgcgtgggg 2929
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     314 AGCTCTTCCTAGCTGGAGAGGAGCCCTGCCTCTCCGCCCCTGAGCCCACTGTGCGTGGGG 255

Qy    2930 ctcccgcctccaacccctcgcccagtcccagcagccagccaaacacacagaaggggactg 2989
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     254 CTCCCGCCTCCAACCCCTCGCCCAGTCCCAGCAGCCAGCCAAACACACAGAAGGGGACTG 195

Qy    2990 ccacctccccttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggg 3049
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     194 CCACCTCCCCTTGCCAGCTGCTGAGCCGCAGAGAAGTGACGGTTCCTACACAGGACAGGG 135

Qy    3050 gttccttctgggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgt 3109
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 GTTCCTTCTGGGCATTACATCGCATAGAAATCAATAATTTGTGGTGATTTGGATCTGTGT 75

Qy    3110 tttaatgagtttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacg 3169
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 TTTAATGAGTTTCACAGTGTGATTTTGATTATTAATTGTGCAAGCTTTTCCTAATAAACG 15

Qy    3170 tggagaatcaca 3181
           ||||||||||||
Db      14 TGGAGAATCACA 3


RESULT  12
AI439544
LOCUS       AI439544      493 bp    mRNA            EST       28-MAR-1999
DEFINITION  tc90b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2073393 3'
            similar to SW:CIK9_MOUSE P97414 VOLTAGE-GATED POTASSIUM CHANNEL
            PROTEIN KV1.9. [1] ;, mRNA sequence.
ACCESSION   AI439544
VERSION     AI439544.1  GI:4305065
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 493)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1584   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 393.
FEATURES              Location/Qualifiers
     source           1. .493
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2073393"
                      /clone_lib="NCI_CGAP_CLL1"
                      /tissue_type="B-cell, chronic lymphotic leukemia"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      Library is normalized, and was constructed by Bento
                      Soares and M.Fatima Bonaldo."
BASE COUNT       64 a    168 c    151 g    110 t
ORIGIN

  Query Match             13.8%;  Score 440;  DB 20;  Length 493;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-209;
  Matches  440;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     405 gcggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccggtgtt 464
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCGGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTT 60

Qy     465 ggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggctggaa 524
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGCGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCCTCGAGCGTCCCACCGGCTGGAA 120

Qy     525 atgcttcgtttaccacttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgt 584
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ATGCTTCGTTTACCACTTCGCCGTCTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGT 180

Qy     585 gctgtccaccatcgagcagtatgccgccctggccacggggactctcttctggatggagat 644
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCTGTCCACCATCGAGCAGTATGCCGCCCTGGCCACGGGGACTCTCTTCTGGATGGAGAT 240

Qy     645 cgtgctggtggtgttcttcgggacggagtacgtggtccgcctctggtccgccggctgccg 704
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CGTGCTGGTGGTGTTCTTCGGGACGGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCG 300

Qy     705 cagcaagtacgtgggcctctgggggcggctgcgctttgcccggaagcccatttccatcat 764
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CAGCAAGTACGTGGGCCTCTGGGGGCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCAT 360

Qy     765 cgacctcatcgtggtcgtggcctccatggtggtcctctgcgtgggctccaaggggcaggt 824
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CGACCTCATCGTGGTCGTGGCCTCCATGGTGGTCCTCTGCGTGGGCTCCAAGGGGCAGGT 420

Qy     825 gtttgccacgtcggccatca 844
           ||||||||||||||||||||
Db     421 GTTTGCCACGTCGGCCATCA 440


RESULT  13
```

```
AW005483/c
LOCUS       AW005483      484 bp    mRNA            EST       08-MAR-2000
DEFINITION  ws94f02.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505627 3'
            similar to contains TAR1.t1 TAR1 repetitive element ;, mRNA
            sequence.
ACCESSION   AW005483
VERSION     AW005483.1  GI:5854261
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 484)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
            , Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arraying: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 685    Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 404.
FEATURES             Location/Qualifiers
     source          1. .484
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2505627"
                     /clone_lib="NCI_CGAP_Co3"
                     /sex="pooled"
                     /tissue_type="colon"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from 12 pooled bulk tumor samples and primed
                     with a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector. Library went through one round of
                     normalization. "
BASE COUNT      108 a    125 c    141 g    110 t
ORIGIN


  Query Match             12.8%;  Score 408;  DB 110;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-193;
  Matches  408;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    2774 tgagcccccagcttccagcaggagggacagtctcaccatttccccagggcacgtggttga 2833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     415 TGAGCCCCCAGCTTCCAGCAGGAGGGACAGTCTCACCATTTCCCCAGGGCACGTGGTTGA 356

Qy    2834 gtgggggaacgcccacttccctgggttagactgccagctcttcctagctggagaggagc 2893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 GTGGGGGGAACGCCCACTTCCCTGGGTTAGACTGCCAGCTCTTCCTAGCTGGAGAGGAGC 296

Qy    2894 cctgcctctccgcccctgagcccactgtgcgtggggctcccgcctccaaccccctcgccca 2953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 CCTGCCTCTCCGCCCCTGAGCCCACTGTGCGTGGGGCTCCCGCCTCCAACCCCTCGCCCA 236

Qy    2954 gtcccagcagccagccaaacacacagaaggggactgccacctccccttgccagctgctga 3013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 GTCCCAGCAGCCAGCCAAACACACAGAAGGGGACTGCCACCTCCCCTTGCCAGCTGCTGA 176

Qy    3014 gccgcagagaagtgacggttcctacacaggacaggggttccttctgggcattacatcgca 3073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 GCCGCAGAGAAGTGACGGTTCCTACACAGGACAGGGGTTCCTTCTGGGCATTACATCGCA 116

Qy    3074 tagaaatcaataatttgtggtgatttggatctgtgttttaatgagtttcacagtgtgatt 3133
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Db     115 TAGAAATCAATAATTTGTGGTGATTTGGATCTGTGTTTTAATGAGTTTCACAGTGTGATT 56

Qy    3134 ttgattattaattgtgcaagcttttcctaataaacgtggagaatcaca 3181
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 TTGATTATTAATTGTGCAAGCTTTTCCTAATAAACGTGGAGAATCACA 8


RESULT  14
BF109081
LOCUS       BF109081      451 bp    mRNA            EST       20-OCT-2000
DEFINITION  7150b06.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
            IMAGE:3524698 3' similar to SW:CIQ1_HUMAN P51787 VOLTAGE-GATED
            POTASSIUM CHANNEL PROTEIN KQT-LIKE 1 ;, mRNA sequence.
ACCESSION   BF109081
VERSION     BF109081.1  GI:10938851
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40UP from Gibco
            High quality sequence stop: 354.
FEATURES             Location/Qualifiers
     source          1. .451
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3524698"
                     /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from five normalized
                     libraries were mixed, and ss circles were made in vitro.
                     Following HAP purification, this DNA was used as tracer in
                     a subtractive hybridization reaction. The driver was
                     PCR-amplified cDNAs from pools of 5,000 clones made from
                     the same 5 libraries. The pools consisted of the following
                     libraries and cloneIDs: Soares NbHSF pool 1:
                     309384-310919, 323208-325895 Soares Nb2HP pool 1:
                     145032-147335, 147720-148103, 148872-149255, 15002 -
                     150407, 151176-152327 Soares Nb2HF8-9W pool 1:
                     758280-760583, 772104-774407 Soares NbHPA pool 1:
                     304776-306311, 320136-322823, 326280-326663 Soares NbHOT
                     pool 1:  723720-726407, 739080-740999 Subtraction by Bento
                     Soares and M. Fatima Bonaldo."
BASE COUNT       62 a    153 c    128 g    108 t
ORIGIN


  Query Match             12.4%;  Score 393;  DB 144;  Length 451;
  Best Local Similarity   100.0%;  Pred. No. 5e-186;
  Matches  393;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     423 agacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtcca 482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTTGGCGCGCACCCACGTCCA 60

Qy     483 gggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccactt 542
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GGGCCGCGTCTACAACTTCCTCGAGCGTCCCACCGGCTGGAAATGCTTCGTTTACCACTT 120
```

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Qy    543 cgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgagca 602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCCGTCTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGTGCTGTCCACCATCGAGCA 180

Qy    603 gtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttctt 662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTATGCCGCCCTGGCCACGGGGACTCTCTTCTGGATGGAGATCGTGCTGGTGGTGTTCTT 240

Qy    663 cgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggcct 722
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGGGACGGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCGCAGCAAGTACGTGGGCCT 300

Qy    723 ctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtcgt 782
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Db    301 CTGGGGGCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCATCGACCTCATCGTGGTCGT 360

Qy    783 ggcctccatggtggtcctctgcgtgggctccaa 815
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Db    361 GGCCTCCATGGTGGTCCTCTGCGTGGGCTCCAA 393


RESULT 15
AI344361
LOCUS       AI344361      418 bp    mRNA            EST       02-FEB-1999
DEFINITION  qp07e12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917358 3'
            similar to SW:CIK9_MOUSE P97414 VOLTAGE-GATED POTASSIUM CHANNEL
            PROTEIN KV1.9. [1] ;, mRNA sequence.
ACCESSION   AI344361
VERSION     AI344361.1  GI:4081567
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 771   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 351.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1917358"
                     /clone_lib="NCI_CGAP_Kid5"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAATATTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT       52 a    144 c    126 g     96 t
ORIGIN
```

```
  Query Match           12.2%;  Score 387;  DB 19;  Length 418;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-183;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    405 gcggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccggtgtt 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTT 60

Qy    465 ggcgcgcacccacgtccagggccgcgtctacaacttcctcgagcgtcccaccggctggaa 524
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCCTCGAGCGTCCCACCGGCTGGAA 120

Qy    525 atgcttcgtttaccacttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgt 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATGCTTCGTTTACCACTTCGCCGTCTTCCTCATCGTCCTGGTCTGCCTCATCTTCAGCGT 180

Qy    585 gctgtccaccatcgagcagtatgccgccctggccacggggactctcttctggatggagat 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCTGTCCACCATCGAGCAGTATGCCGCCCTGGCCACGGGGACTCTCTTCTGGATGGAGAT 240

Qy    645 cgtgctggtggtgttcttcgggacggagtacgtggtccgcctctggtccgccggctgccg 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGTGCTGGTGGTGTTCTTCGGGACGGAGTACGTGGTCCGCCTCTGGTCCGCCGGCTGCCG 300

Qy    705 cagcaagtacgtgggcctctgggggcggctgcgctttgcccggaagcccatttccatcat 764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CAGCAAGTACGTGGGCCTCTGGGGGCGGCTGCGCTTTGCCCGGAAGCCCATTTCCATCAT 360

Qy    765 cgacctcatcgtggtcgtggcctccat 791
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Db    361 CGACCTCATCGTGGTCGTGGCCTCCAT 387


Search completed: November  2, 2001, 13:28:40
Job time: 4736 sec
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GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 12:12:04 ; Search time 294.94 Seconds
(without alignments)
6772.072 Million cell updates/sec

Title: US-09-135-010A-1
Perfect score: 3181
Sequence: 1 ctgccccctccggccccgcc.....aataaacgtggagaatcaca 3181

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 730101 seqs, 313950809 residues

Word size : 12

Total number of hits satisfying chosen parameters: 106307

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_0601:*
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22: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 3181 | 100.0 | 3181 | 21 | AAZ90669 | Human KVLQT1 prote |
| | 2 | 3181 | 100.0 | 3181 | 21 | AAZ98901 | Human long QT synd |
| | 3 | 3181 | 100.0 | 3181 | 22 | AAC89911 | Human KVLQT1 codin |
| | 4 | 3061 | 96.2 | 3182 | 22 | AAC89914 | Mutant human KVLQT |
| | 5 | 2702 | 84.9 | 2734 | 22 | AAC89984 | Mutant human KVLQT |
| | 6 | 2702 | 84.9 | 2821 | 18 | AAT94004 | DNA encoding human |
| | 7 | 2702 | 84.9 | 2821 | 18 | AAT90730 | Human KVLQT1 full- |
| | 8 | 265 | 8.3 | 494 | 21 | AAC98925 | Human pancreatic c |
| | 9 | 159 | 5.0 | 432 | 21 | AAC98263 | Human colon cancer |
| c | 10 | 96 | 3.0 | 2821 | 18 | AAT94004 | DNA encoding human |
| c | 11 | 96 | 3.0 | 2821 | 18 | AAT90730 | Human KVLQT1 full- |
| | 12 | 45 | 1.4 | 45 | 20 | AAZ11946 | Human potassium ch |
| | 13 | 41 | 1.3 | 83 | 16 | AAT26420 | Human gene signatu |
| c | 14 | 34 | 1.1 | 2734 | 22 | AAC89984 | Mutant human KVLQT |
| | 15 | 22 | 0.7 | 22 | 18 | AAT91065 | Human KVLQT1 S2-S3 |
| | 16 | 22 | 0.7 | 22 | 18 | AAT90717 | Human KVLQT1 S2-S3 |
| | 17 | 22 | 0.7 | 22 | 21 | AAZ90741 | Human KVLQT1 mutat |
| | 18 | 22 | 0.7 | 22 | 21 | AAZ98971 | Mutant human long |
| | 19 | 21 | 0.7 | 2335 | 21 | AAA47618 | KCNQ4 Potassium ch |
| | 20 | 21 | 0.7 | 910715 | 20 | AAX20248 | Borrelia burgdorfe |
| | 21 | 20 | 0.6 | 20 | 18 | AAT91069 | Human KVLQT1 S4 re |
| | 22 | 20 | 0.6 | 20 | 18 | AAT90721 | Human KVLQT1 S4 re |
| | 23 | 20 | 0.6 | 20 | 21 | AAZ90745 | Human KVLQT1 mutat |
| | 24 | 20 | 0.6 | 20 | 21 | AAZ98975 | Mutant human long |
| | 25 | 20 | 0.6 | 936 | 20 | AAX56375 | Human DNA-dependen |
| c | 26 | 20 | 0.6 | 2065 | 19 | AAV29062 | BRCA1 modulator pr |
| c | 27 | 20 | 0.6 | 2065 | 20 | AAX86754 | cDNA 091-21A31 enc |
| | 28 | 19 | 0.6 | 19 | 21 | AAZ90707 | Forward primer for |
| c | 29 | 19 | 0.6 | 19 | 21 | AAZ90708 | Reverse primer for |
| | 30 | 19 | 0.6 | 19 | 21 | AAZ98937 | Human long QT synd |
| c | 31 | 19 | 0.6 | 19 | 21 | AAZ98938 | Human long QT synd |
| | 32 | 19 | 0.6 | 19 | 22 | AAC89947 | Human KVLQTI exon |
| c | 33 | 19 | 0.6 | 19 | 22 | AAC89948 | Human KVLQTI exon |
| c | 34 | 19 | 0.6 | 263 | 21 | AAC24694 | Human secreted pro |
| c | 35 | 19 | 0.6 | 770 | 20 | AAV88894 | EST clone HZ162. |
| | 36 | 19 | 0.6 | 1182 | 21 | AAA27105 | Human h-TRAAK cDNA |
| | 37 | 19 | 0.6 | 1218 | 21 | AAA27106 | Human h-TRAAK cDNA |
| | 38 | 19 | 0.6 | 1323 | 21 | AAC74299 | Human secreted pro |
| | 39 | 19 | 0.6 | 1678 | 21 | AAC99026 | Human pancreatic c |
| c | 40 | 19 | 0.6 | 1765 | 22 | AAF93864 | Human cDNA encodin |
| | 41 | 19 | 0.6 | 2786 | 16 | AAT06023 | cDNA encoding aven |
| | 42 | 19 | 0.6 | 3269 | 16 | AAT06024 | cDNA encoding aven |
| | 43 | 19 | 0.6 | 4132 | 20 | AAX60265 | Nucleic acid seque |
| | 44 | 19 | 0.6 | 6910 | 21 | AAA38335 | Human aldosterone |
| c | 45 | 19 | 0.6 | 7011 | 19 | AAV20464 | Human L-myc oncoge |

ALIGNMENTS

RESULT 1
AAZ90669
ID AAZ90669 standard; cDNA; 3181 BP.
XX
AC AAZ90669;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human KVLQT1 protein encoding cDNA.
XX
KW KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
KW antiarrhythmic; gene therapy; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 163..2193
FT /*tag= a
FT /product= "KVLQT1"
XX
PN WO200006600-A1.
XX
PD 10-FEB-2000.
XX
PF 06-OCT-1998; 98WO-US17838.
XX
PR 29-JUL-1998; 98US-0094477.
PR 17-AUG-1998; 98US-0135020.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Keating MT, Sanguinetti MC, Splawski I;
XX
DR WPI; 2000-195262/17.

DR P-PSDB; AAY57368.
XX
PT Mutant forms of genes encoding minK protein and KVLQT1 protein involved
PT in cardiac potassium channel formation useful for screening drugs, for
PT preventing and treating cardiac arrhythmia -
XX
PS Claim 28; Fig 5A-B; 167pp; English.
XX
CC The invention relates to KVLQT1 and KCNE1 genes, associated with long
CC QT (LQT) syndrome. It provides a minK protein comprising a mutation which
CC substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
CC Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening
CC KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
CC treating LQT. The ability to predict LQT enables physicians to prevent
CC the diseases with medical therapy such as beta blocking agents and opts
CC for better treatments. The present sequence represents the cDNA encoding
CC the human KVLQT1 protein.
XX
SQ Sequence 3181 BP; 581 A; 1073 C; 968 G; 559 T; 0 other;

Query Match 100.0%; Score 3181; DB 21; Length 3181;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120
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Db      61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120

Qy     121 gtgccgccgctcgggccggcccccccggcaggccctcctcgttatggccgcggcctcctcc 180
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Qy     181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240
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Qy     241 agcgcgggcctggccaagaagtgccccttctcgctggagctggcggagggcggcccggcg 300
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Qy     301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgccccctgcgtcc 360
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Qy     361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420
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Db     361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420

Qy     421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480
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Qy     481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540
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Qy     541 ttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgag 600
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Qy     601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660

Qy     661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720
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Db     661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720

Qy     721 ctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtc 780
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Db     721 ctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtc 780

Qy     781 gtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggcc 840
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Qy     841 atcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggc 900
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Qy     901 acctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctg 960
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Qy    1081 gtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaag 1140
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Qy    1381 tcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggac 1440
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Db    1441 aaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgac 1500

Qy    1501 cccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaagg 1560
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Qy    2821 ggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttccta 2880
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Qy    2881 gctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctcc 2940
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Qy    3121 tcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatcac 3180
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Qy    3181 a 3181
Db    3181 a 3181
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RESULT 2
AAZ98901
ID AAZ98901 standard; cDNA; 3181 BP.
XX
AC AAZ98901;
XX
DT 06-JUN-2000 (first entry)
XX
DE Human long QT syndrome-associated KVLQT1 cDNA.
XX
KW KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss;
KW cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
KW chromosome 11p15.5.
XX
OS Homo sapiens.
XX
PN WO200006199-A1.
XX
PD 10-FEB-2000.
XX
PF 12-MAY-1999; 99WO-US10260.
XX
PR 29-JUL-1998; 98US-0094477.
PR 17-AUG-1998; 98US-0135010.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
PA (GENZ ) GENZYME CORP.
XX
PI Keating MT, Sanguinetti MC, Curran ME, Landes GM, Connors TD;
PI Burn TC, Splawski I;
XX
DR WPI; 2000-195199/17.
DR P-PSDB; AAY80562.
XX
PT New isolated mutant KVLQT1 nucleic acids, useful for developing
PT products for the diagnosis, prevention and treatment of long QT
PT syndrome -
XX
PS Claim 1; Fig 5A-B; 178pp; English.
XX
CC The invention relates to KVLQT1 nucleic acids which have a mutation
CC compared to wild-type KVLQT1. This sequence corresponds to the human
CC wild type KVLQT1 cDNA sequence. The sequence encodes a protein of 676
CC amino acid which forms a cardiac I(ks) potassium channel with the KCNE1
CC protein (AAY80563). The KVLQT1 gene contains 15 introns and encodes a
CC protein containing 6 putative transmembrane segments and a pore forming
CC region. The gene has been mapped to the chromosomal location 11p15.5.
CC Mutations in the KVLQT1 or KCNE1 genes result in cardiac arrhythmias
CC observed as a prolonged QT curve in electrocardiograms (Long QT
CC syndrome). The genes and proteins can be used for the diagnosis of

CC subjects with long QT syndrome. They can also be used to screen for
CC drugs which can be used for treating or preventing long QT syndrome.
CC The KVLQT1 nucleic acids can be used for gene therapy, and KVLQT1
CC peptides can be used for peptide therapy.
XX
SQ Sequence 3181 BP; 581 A; 1073 C; 968 G; 559 T; 0 other;

Query Match 100.0%; Score 3181; DB 21; Length 3181;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 ctgccccctccggccccgccccgagcgcccgggctgggccggcagcggccccccgcggcg 60

Qy      61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120
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Qy     121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180
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Qy     181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240
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Qy     301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgccccctgcgtcc 360
Db     301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgccccctgcgtcc 360

Qy     361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420
Db     361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420

Qy     421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480
Db     421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480

Qy     481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540
Db     481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540

Qy     541 ttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgag 600
Db     541 ttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgag 600

Qy     601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660
Db     601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660

Qy     661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720
Db     661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720

Qy     721 ctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtc 780
Db     721 ctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtc 780

Qy     781 gtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggcc 840
Db     781 gtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggcc 840

Qy     841 atcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggc 900
Db     841 atcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggc 900

Qy     901 acctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctg 960
Db     901 acctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctg 960

Qy     961 tacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggac 1020
Db     961 tacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggac 1020

Qy    1021 gcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtggggg 1080
Db    1021 gcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtggggg 1080

Qy    1081 gtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaag 1140
Db    1081 gtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaag 1140

Qy    1141 accatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggatt 1200
Db    1141 accatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggatt 1200

Qy    1201 cttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccgg 1260
Db    1201 cttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccgg 1260

Qy    1261 cagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaac 1320
Db    1261 cagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaac 1320

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Qy    1381 tcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggac 1440
Db    1381 tcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggac 1440

Qy    1441 aaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgac 1500
Db    1441 aaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgac 1500

Qy    1501 cccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaagg 1560
Db    1501 cccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaagg 1560

Qy    1561 aagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgcc 1620
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Qy    1621 gaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagctg 1680
Db    1621 gaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagctg 1680

Qy    1681 cgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaag 1740
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Qy    1741 aagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcg 1800
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Qy    1801 cagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtcc 1860
Db    1801 cagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtcc 1860

Qy    1861 attgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaac 1920
Db    1861 attgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaac 1920

Qy    1921 acgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctg 1980
Db    1921 acgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctg 1980

Qy    1981 gcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccggc 2040
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Qy   2041 agcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcggc 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2101 tccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgacc 2160
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Qy   2161 gtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcc 2220
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Qy   2221 tgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctcc 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2281 taaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgct 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 taaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgct 2340
Qy   2341 gtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggg 2400
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Db   2341 gtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggg 2400
Qy   2401 gccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttga 2460
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Qy   2461 catcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggc 2520
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Qy   2521 caggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgagg 2580
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Qy   2581 ggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcag 2640
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Qy   2641 ggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccattt 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2701 ggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactg 2760
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Qy   2761 tggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccag 2820
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Qy   2821 ggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttccta 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2881 gctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctcc 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 gctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctcc 2940
Qy   2941 aacccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccct 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3001 tgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgg 3060
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Qy   3061 gcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagtt 3120
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Qy   3121 tcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatcac 3180
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Db   3121 tcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatcac 3180

Qy   3181 a 3181
          |
Db   3181 a 3181
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RESULT 3
AAC89911
ID AAC89911 standard; cDNA; 3181 BP.
XX
AC AAC89911;
XX
DT 08-MAR-2001 (first entry)
XX
DE Human KVLQT1 coding sequence.
XX
KW Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW chromosome 11p15.5; long QT syndrome; ss.
XX
OS Homo sapiens.
XX
PN US6150104-A.
XX
PD 21-NOV-2000.
XX
PF 17-AUG-1998; 98US-0135021.
XX
PR 29-JUL-1998; 98US-0094477.
PR 13-JUN-1997; 97US-0874655.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Keating MT.; Splawski I;
XX
DR WPI; 2001-060013/07.
DR P-PSDB; AAB49494.
XX
PT DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT or diagnosing or prognosing JLN -
XX
PS Example 4; Columns 53-60; 58pp; English.
XX
CC The present sequence is the coding sequence for wild-type human KVLQT1.
CC KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
CC chromosome 11p15.5. The present invention relates to a mutant KVLQT1
CC coding sequence (see AAC89914). The mutant KVLQT1 coding sequence is
CC useful in the diagnosis of long QT syndrome and in screening humans for
CC the presence of KVLQT1 gene variants which cause JLN syndrome.
XX
SQ Sequence 3181 BP; 581 A; 1073 C; 968 G; 559 T; 0 other;

```
  Query Match            100.0%;  Score 3181;  DB 22;  Length 3181;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ctgccccctccggccccgccccgagcgcccgggctgggccggcagcggccccccgcggcg 60
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Qy      61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120
Qy     121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180
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Db    121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180

Qy    181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240

Qy    241 agcgcgggcctggccaagaagtgccccttctcgctggagctggcggagggcggcccggcg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 agcgcgggcctggccaagaagtgccccttctcgctggagctggcggagggcggcccggcg 300

Qy    301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgccccctgcgtcc 360
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Qy    361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420

Qy    421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480
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Qy    481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540
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Db    481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540

Qy    541 ttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgag 600
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Qy    601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660
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Qy    661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720
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Qy    721 ctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggtc 780
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Qy    781 gtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggcc 840
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Qy    841 atcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggaggc 900
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Qy    901 acctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccctg 960
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Qy    961 tacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaaggac 1020
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Qy   1021 gcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtggggg 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1081 gtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaag 1140
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Qy   1141 accatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggatt 1200
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Qy   1201 cttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccgg 1260
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Qy   1261 cagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaac 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 cagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaac 1320

Qy   1321 cccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgctg 1380
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Qy   1381 tcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggac 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 tcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctggac 1440

Qy   1441 aaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcgac 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1501 cccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaagg 1560
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Qy   1561 aagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgcc 1620
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Qy   1681 cgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaag 1740
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Db   1681 cgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaag 1740

Qy   1741 aagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcg 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 aagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactcg 1800

Qy   1801 cagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtcc 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 cagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtcc 1860

Qy   1861 attgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaac 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 attgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaac 1920

Qy   1921 acgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctg 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 acgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggctg 1980

Qy   1981 gcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcaccccggc 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 gcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcaccccggc 2040

Qy   2041 agcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcggc 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 agcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcggc 2100

Qy   2101 tccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgacc 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 tccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgacc 2160

Qy   2161 gtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcc 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 gtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggcc 2220

Qy   2221 tgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctcc 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 tgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctcc 2280

Qy   2281 taaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgct 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 taaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgct 2340
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Qy   2341 gtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggg 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 gtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtgggg 2400

Qy   2401 gccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttga 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 gccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttga 2460

Qy   2461 catcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggc 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 catcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatggc 2520

Qy   2521 caggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgagg 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 caggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgagg 2580

Qy   2581 ggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcag 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 ggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggcag 2640

Qy   2641 ggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccattt 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 ggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccattt 2700

Qy   2701 ggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactg 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 ggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagactg 2760

Qy   2761 tggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccag 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 tggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccag 2820

Qy   2821 ggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttccta 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 ggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttccta 2880

Qy   2881 gctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctcc 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 gctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctcc 2940

Qy   2941 aacccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctccccct 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 aacccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctccccct 3000

Qy   3001 tgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgg 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 tgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctgg 3060

Qy   3061 gcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagtt 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 gcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagtt 3120

Qy   3121 tcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatcac 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 tcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatcac 3180

Qy   3181 a 3181
          |
Db   3181 a 3181
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RESULT 4
AAC89914
ID AAC89914 standard; cDNA; 3182 BP.
XX
AC AAC89914;
XX
DT 08-MAR-2001 (first entry)
XX
DE Mutant human KVLQT1 coding sequence #2.
XX
KW Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW chromosome 11p15.5; long QT syndrome; ss.
XX
OS Homo sapiens.
XX
PN US6150104-A.
XX
PD 21-NOV-2000.
XX
PF 17-AUG-1998; 98US-0135021.
XX
PR 29-JUL-1998; 98US-0094477.
PR 13-JUN-1997; 97US-0874655.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Keating MT; Splawski I;
XX
DR WPI; 2001-060013/07.
DR P-PSDB; AAB49495.
XX
PT DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT or diagnosing or prognosing JLN -
XX
PS Example 4; Columns 63-68; 58pp; English.
XX
CC KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
CC chromosome 11p15.5. The present sequence is a mutant KVLQT1 coding
CC sequence. The mutant KVLQT1 coding sequence is useful in the diagnosis of
CC long QT syndrome and in screening humans for the presence of KVLQT1 gene
CC variants which cause JLN syndrome.
XX
SQ Sequence 3182 BP; 581 A; 1073 C; 969 G; 559 T; 0 other;

Query Match 96.2%; Score 3061; DB 22; Length 3182;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3181; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      1 ctgccccctccggccccgccccgagcgcccgggctgggccggcagcggccccccgcggcg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ctgccccctccggccccgccccgagcgcccgggctgggccggcagcggccccccgcggcg 60

Qy     61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 gggctggcagcagtggctgcccgcactgcgcccgggcgctcgccttcgctgcagctcccg 120

Qy    121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gtgccgccgctcgggccggccccccggcaggccctcctcgttatggccgcggcctcctcc 180

Qy    181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ccgcccagggccgagaggaagcgctggggttggggccgcctgccaggcgcccggcggggc 240

Qy    241 agcgcgggcctggccaagaagtgccccttctcgctggagctggcggagggcggcccggcg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 agcgcgggcctggccaagaagtgccccttctcgctggagctggcggagggcggcccggcg 300

Qy    301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgccccctgcgtcc 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ggcggcgcgctctacgcgcccatcgcgcccggcgccccaggtcccgcgccccctgcgtcc 360

Qy    361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ccggccgcgcccgccgcgcccccagttgcctccgaccttggcccgcggccgccggtgagc 420

Qy    421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ctagacccgcgcgtctccatctacagcacgcgccgcccggtgttggcgcgcacccacgtc 480

Qy    481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540
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Db    481 cagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttaccac 540
Qy    541 ttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgag 600
Db    541 ttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcgag 600
Qy    601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660
Db    601 cagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgttc 660
Qy    661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720
Db    661 ttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggc 720
Qy    721 ctct-gggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 779
Db    721 ctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 780
Qy    780 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 839
Db    781 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 840
Qy    840 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 899
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Qy    900 cacctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccct 959
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Qy    960 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 1019
Db    961 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 1020
Qy   1020 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 1079
Db   1021 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 1080
Qy   1080 ggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaa 1139
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Qy   1140 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 1199
Db   1141 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 1200
Qy   1200 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1259
Db   1201 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1260
Qy   1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
Db   1261 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1320
Qy   1320 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 1379
Db   1321 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 1380
Qy   1380 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 1439
Db   1381 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaagttcaagctgga 1440
Qy   1440 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1499
Db   1441 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1500
Qy   1500 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1559
Db   1501 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1560
Qy   1560 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1619
Db   1561 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1620
Qy   1620 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1679
Db   1621 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1680
Qy   1680 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1739
Db   1681 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1740
Qy   1740 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1799
Db   1741 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1800
Qy   1800 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1859
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Qy   1860 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1919
Db   1861 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1920
Qy   1920 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1979
Db   1921 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1980
Qy   1980 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 2039
Db   1981 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 2040
Qy   2040 cagcggcggccccccagagagggcgggggcccacatcacccagccctgcggcagtggcgg 2099
Db   2041 cagcggcggccccccagagagggcgggggcccacatcacccagccctgcggcagtggcgg 2100
Qy   2100 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 2159
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Qy   2160 cgtgcccaggagggggccccgatgaggggtcctgaggaggggatggggctgggggatgggc 2219
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Qy   2520 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccagggggcttcctgag 2579
Db   2521 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccagggggcttcctgag 2580
Qy   2580 gggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggca 2639
Db   2581 gggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggca 2640
Qy   2640 gggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatt 2699
Db   2641 gggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatt 2700
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Qy   2700 tggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagact 2759
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Db   2701 tggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagact 2760

Qy   2760 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttcccca 2819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttcccca 2820

Qy   2820 gggcacgtggttgagtgggggaacgcccacttccctgggttagactgccagctcttcct 2879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 gggcacgtggttgagtgggggaacgcccacttccctgggttagactgccagctcttcct 2880

Qy   2880 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2940

Qy   2940 caacccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 caacccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 3000

Qy   3000 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 3060

Qy   3060 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 3119
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Qy   3120 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 3179
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Qy   3180 ca 3181
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Db   3181 ca 3182
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RESULT 5
AAC89984
ID AAC89984 standard; cDNA; 2734 BP.
XX
AC AAC89984;
XX
DT 08-MAR-2001 (first entry)
XX
DE Mutant human KVLQT1 coding sequence #1.
XX
KW Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW chromosome 11p15.5; long QT syndrome; ss.
XX
OS Homo sapiens.
XX
PN US6150104-A.
XX
PD 21-NOV-2000.
XX
PF 17-AUG-1998; 98US-0135021.
XX
PR 29-JUL-1998; 98US-0094477.
PR 13-JUN-1997; 97US-0874655.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Keating MT; Splawski I;
XX
DR WPI; 2001-060013/07.
DR P-PSDB; AAB49499.
XX
PT DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT or diagnosing or prognosing JLN -
XX
PS Claim 2; Columns 91-96; 58pp; English.
XX
CC KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
CC chromosome 11p15.5. The present sequence is a mutant KVLQT1 coding
CC sequence. The mutant KVLQT1 coding sequence is useful in the diagnosis of
CC long QT syndrome and in screening humans for the presence of KVLQT1 gene
CC variants which cause JLN syndrome.
XX
SQ Sequence 2734 BP; 551 A; 864 C; 809 G; 510 T; 0 other;

Query Match 84.9%; Score 2702; DB 22; Length 2734;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    480 ccagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttacca 539
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Qy    540 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 599
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Qy    600 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 659
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Qy    660 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtggg 719
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Qy    720 cctctgggggcggctgcgctttgcccggaagcccatttccatcatcgacctcatcgtggt 779
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Qy    780 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 839
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Qy    840 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 899
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Db    393 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 452

Qy    900 cacctggaggctcctgggctccgtggtcttcatccaccgccaggagctgataaccaccct 959
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Qy    960 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 1019
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Qy   1020 cgcggtgaacgagtcaggccgcgtggagttcggcagctacgcagatgcgctgtggtgggg 1079
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Qy   1080 ggtggtcacagtcaccaccatcggctatggggacaaggtgccccagacgtgggtcgggaa 1139
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Qy   1140 gaccatcgcctcctgcttctctgtctttgccatctccttctttgcgctcccagcggggat 1199
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Qy   1200 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1259
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Qy   1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
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Qy   1380 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 1439
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Qy   1500 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1559
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Qy   1560 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1619
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Qy   1620 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1679
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Qy   1680 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1739
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Qy   1800 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1859
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Qy   1860 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1919
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Qy   1920 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1979
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Qy   1980 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 2039
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Qy   2040 cagcggcggcccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 2099
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Qy   2100 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 2159
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Qy   2160 cgtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggc 2219
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Qy   2220 ctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctc 2279
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Qy   2280 ctaaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgc 2339
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Qy   2640 gggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatt 2699
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Qy   2760 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttcccca 2819
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Qy   2820 gggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcct 2879
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Qy   2940 caacccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2999
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Qy   3120 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 3179
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Qy   3180 ca 3181
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Db   2733 ca 2734
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RESULT 6
AAT94004
ID AAT94004 standard; DNA; 2821 BP.
XX
AC AAT94004;
XX
DT 28-FEB-1998 (first entry)
XX
DE DNA encoding human KVLQT1.
XX
KW KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW diagnosis; therapy; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 88..1833

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FT                    /*tag= a
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PN   WO9723632-A1.
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PD   03-JUL-1997.
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PF   20-DEC-1996;   96WO-US19917.
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PR   29-OCT-1996;   96US-0739383.
PR   22-DEC-1995;   95US-0019014.
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PA   (GENZ ) GENZYME GENETICS.
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Connors TD,  Curran ME,  Keating MF,  Landes GM;
XX
DR   WPI; 1997-402191/37.
DR   P-PSDB; AAW33355.
XX
PT   New isolated human potassium channel gene, KVLQT1, - used to develop
PT   products for diagnosis, prevention and therapy of long QT syndrome
XX
PS   Claim 2; Page 76-79; 117pp; English.
XX
CC   This cDNA sequence includes a full-length coding sequence for human
CC   KVLQT1 (see AAW33355), a novel cardiac potassium channel protein.
CC   The sequence was assembled from partial clones isolated from human
CC   pancreatic and cardiac cDNA libraries.  KVLQT1 was mapped to
CC   chromosome 11p15.5 making it a candidate for the long QT syndrome
CC   (LQT) gene.  LQT is an inherited cardiac arrhythmia.  16 Families
CC   with mutations in KVLQT1 have been identified and it was shown that
CC   in all 16 families there was complete linkage between LQT1 and
CC   KVLQT1.  The KVLQT1 gene product coassembles with human minK to
CC   form a cardiac IKs potassium channel.  IKs dysfunction is a cause
CC   of cardiac arrhythmia.  Coexpression of KVLTQ1 and minK in a host
CC   cell provides a means for screening for drugs useful in treating or
CC   preventing LQT.  Analysis of the KVLQT1 gene will provide an early
CC   diagnosis of subjects with LQT.  A claimed method of assessing the
CC   risk in a human for LQT syndrome comprises screening for a mutation
CC   in the KVLQT1 gene.  Transgenic animals expressing human minK and
CC   KVQLT1 can be used to test therapeutic agents against LQT.
XX
SQ   Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;


  Query Match             84.9%;  Score 2702;  DB 18;  Length 2821;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2702;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     540 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 599
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Qy     600 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 659
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Qy     780 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 839
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Qy     840 catcaggggcatccgcttcctgcagatcctgaggatgctacacgtcgaccgccagggagg 899
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Qy    1200 tcttggctcgggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1259
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Qy    1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
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Qy    1320 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 1379
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Qy    1380 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 1439
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Qy    1440 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1499
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Qy    1500 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1559
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Qy    1560 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1619
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1680 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1800 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1859
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Qy    1860 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1919
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    1920 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1979
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Qy   3180 ca 3181
          ||
Db   2820 ca 2821
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RESULT 7
AAT90730
ID AAT90730 standard; cDNA; 2821 BP.
XX
AC AAT90730;
XX
DT 12-FEB-1998 (first entry)
XX
DE Human KVLQT1 full-length cDNA.
XX
KW KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW diagnosis; therapy; human; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 88..1833
FT /*tag= a
XX
PN WO9723598-A2.
XX
PD 03-JUL-1997.
XX
PF 20-DEC-1996; 96WO-US19756.
XX
PR 29-OCT-1996; 96US-0739383.
PR 22-DEC-1995; 95US-0019014.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Curran ME, Keating MT, Sanguinetti MC;
XX
DR WPI; 1997-402190/37.
DR P-PSDB; AAW30038.
XX
PT Human minK and Xenopus KVLQT1 coding sequences - used for assays for
PT identifying drugs which can be used for preventing or treating long
PT QT syndrome
XX
PS Example 9; Page 76-79; 105pp; English.
XX
CC This cDNA sequence includes a full-length coding sequence for human
CC KVLQT1 (see AAW30038), a novel cardiac potassium channel protein.
CC The sequence was assembled from partial clones isolated from human
CC pancreatic and cardiac cDNA libraries. KVLQT1 was mapped to
CC chromosome 11p15.5 making it a candidate for the long QT syndrome
CC (LQT) gene. LQT is an inherited cardiac arrhythmia. One intragenic
CC deletion and 10 different missense mutations which cause LQT have
CC been identified in KVLQT1. The KVLQT1 gene product coassembles
CC with human minK to form a cardiac IKs potassium channel.
CC Coexpression of these 2 proteins in a host cell provides a means
CC for screening for drugs useful in treating or preventing LQT. The
CC products can also be used for studying mechanisms underlying common
CC arrhythmias and for presymptomatic diagnosis of LQT. Transgenic
CC animals expressing human minK and KVQLT1 can be used to test
CC therapeutic agents against LQT.
XX
SQ Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

Query Match 84.9%; Score 2702; DB 18; Length 2821;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    480 ccagggccgcgtctacaacttcctcgagcgtcccaccggctggaaatgcttcgtttacca 539
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Qy    540 cttcgccgtcttcctcatcgtcctggtctgcctcatcttcagcgtgctgtccaccatcga 599
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Qy    600 gcagtatgccgccctggccacggggactctcttctggatggagatcgtgctggtggtgtt 659
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Qy    660 cttcgggacggagtacgtggtccgcctctggtccgccggctgccgcagcaagtacgtgggg 719
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Qy    780 cgtggcctccatggtggtcctctgcgtgggctccaaggggcaggtgtttgccacgtcggc 839
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Qy    960 gtacatcggcttcctgggcctcatcttctcctcgtactttgtgtacctggctgagaagga 1019
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Qy   1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
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Qy   2520 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccaggggggcttcctgag 2579
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2460 gggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcct 2519

Qy   2880 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2520 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2579

Qy   2940 caaccccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2580 caaccccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2639

Qy   3000 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2640 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 2699

Qy   3060 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2700 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 2759

Qy   3120 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2760 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 2819

Qy   3180 ca 3181
          ||
Db   2820 ca 2821
```

RESULT 8
AAC98925
ID AAC98925 standard; cDNA; 494 BP.
XX
AC AAC98925;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:153.
XX
KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW nootropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic;
KW neural; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative; ss.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05989.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-579444/54.
DR P-PSDB; AAB54160.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
PS Claim 1; Page 610-611; 1379pp; English.
XX
CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 494 BP; 120 A; 149 C; 147 G; 74 T; 4 other;

Query Match 8.3%; Score 265; DB 21; Length 494;
Best Local Similarity 99.7%; Pred. No. 2.7e-110;
Matches 315; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy   1600 atgagaaccaacagcttcgccgaggacctggacctggaaggggagactctgctgacaccc 1659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 atgagaaccaacagcttcgccgaggacctggacctggaaggggagactctgctgacaccc 60

Qy   1660 atcacccacatctcacagctgcgggaacaccatcgggccaccattaaggtcattcgacgc 1719
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     61 atcacccacatctcacagctgcgggaacaccatcgggccaccattaaggtcattngacgc 120

Qy   1720 atgcagtactttgtggccaagaagaaattccagcaagcgcggaagccttacgatgtgcgg 1779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 atgcagtactttgtggccaagaagaaattccagcaagcgcggaagccttacgatgtgcgg 180

Qy   1780 gacgtcattgagcagtactcgcagggccacctcaacctcatggtgcgcatcaaggagctg 1839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 gacgtcattgagcagtactcgcagggccacctcaacctcatggtgcgcatcaaggagctg 240

Qy   1840 cagaggaggctggaccagtccattgggaagccctcactgttcatctccgtctcagaaaag 1899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 cagaggaggctggaccagtccattgggaagccctcactgttcatctccgtctcagaaaag 300

Qy   1900 agcaaggatcgcggca 1915
          ||||||||||||||||
Db    301 agcaaggatcgcggca 316
```

RESULT 9
AAC98263
ID AAC98263 standard; cDNA; 432 BP.
XX
AC AAC98263;

```
XX
DT   09-MAR-2001  (first entry)
XX
DE   Human colon cancer antigen nucleotide sequence SEQ ID NO:273.
XX
KW   Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW   identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW   immunomodulatory; muscular; gynaecological; gastrointestinal;
KW   nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW   neural disorder; immune system disorder; muscular disorder;
KW   reproductive disorder; gastrointestinal disorder; renal disorder;
KW   infectious disease; cardiovascular disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200055351-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US05883.
XX
PR   12-MAR-1999;   99US-0124270.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587534/55.
DR   P-PSDB; AAB53506.
XX
PT   Colon cancer associated gene sequences, referred to as colon cancer
PT   antigens, useful for the treatment, prevention, and diagnosis of colon
PT   disorders such as colon cancer -
XX
PS   Claim 1; Page 698-699; 2104pp; English.
XX
CC   AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC   called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC   human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC   neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC   vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC   can be used in gene therapy. The colon cancer antigen polynucleotides,
CC   proteins and antibodies to the proteins are useful for the prevention,
CC   treatment and diagnosis of colon disorders, such as colon cancer. The
CC   polynucleotides may be used in diagnostics and research, such as for
CC   chromosome identification, and as hybridisation probes. The proteins
CC   may also be used to prevent diseases such as neural disorders, immune
CC   system disorders, muscular disorders, reproductive disorders,
CC   gastrointestinal disorders, wounds, renal disorders, infectious
CC   diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC   AAB54007 represent sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 432 BP; 105 A; 120 C; 109 G; 90 T; 8 other;


  Query Match             5.0%;  Score 159;  DB 21;  Length 432;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-62;
  Matches  159;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1878 gttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacgatcggcgcccgcct 1937
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2 gttcatctccgtctcagaaaagagcaaggatcgcggcagcaacacgatcggcgcccgcct 61

Qy    1938 gaaccgagtagaagacaaggtgacgcagctggaccagaggctggcactcatcaccgacat 1997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      62 gaaccgagtagaagacaaggtgacgcagctggaccagaggctggcactcatcaccgacat 121

Qy    1998 gcttcaccagctgctctccttgcacggtggcagcacccc 2036
           |||||||||||||||||||||||||||||||||||||||
Db     122 gcttcaccagctgctctccttgcacggtggcagcacccc 160
```

```
RESULT  10
AAT94004/c
ID   AAT94004 standard; DNA; 2821 BP.
XX
AC   AAT94004;
XX
DT   28-FEB-1998  (first entry)
XX
DE   DNA encoding human KVLQT1.
XX
KW   KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW   diagnosis; therapy; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             88..1833
FT                   /*tag=  a
XX
PN   WO9723632-A1.
XX
PD   03-JUL-1997.
XX
PF   20-DEC-1996;   96WO-US19917.
XX
PR   29-OCT-1996;   96US-0739383.
PR   22-DEC-1995;   95US-0019014.
XX
PA   (GENZ ) GENZYME GENETICS.
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Connors TD,  Curran ME,  Keating MF,  Landes GM;
XX
DR   WPI; 1997-402191/37.
DR   P-PSDB; AAW33355.
XX
PT   New isolated human potassium channel gene, KVLQT1, - used to develop
PT   products for diagnosis, prevention and therapy of long QT syndrome
XX
PS   Claim 2; Page 76-79; 117pp; English.
XX
CC   This cDNA sequence includes a full-length coding sequence for human
CC   KVLQT1 (see AAW33355), a novel cardiac potassium channel protein.
CC   The sequence was assembled from partial clones isolated from human
CC   pancreatic and cardiac cDNA libraries.  KVLQT1 was mapped to
CC   chromosome 11p15.5 making it a candidate for the long QT syndrome
CC   (LQT) gene.  LQT is an inherited cardiac arrhythmia.  16 Families
CC   with mutations in KVLQT1 have been identified and it was shown that
CC   in all 16 families there was complete linkage between LQT1 and
CC   KVLQT1.  The KVLQT1 gene product coassembles with human minK to
CC   form a cardiac IKs potassium channel.  IKs dysfunction is a cause
CC   of cardiac arrhythmia.  Coexpression of KVLTQ1 and minK in a host
CC   cell provides a means for screening for drugs useful in treating or
CC   preventing LQT.  Analysis of the KVLQT1 gene will provide an early
CC   diagnosis of subjects with LQT.  A claimed method of assessing the
CC   risk in a human for LQT syndrome comprises screening for a mutation
CC   in the KVLQT1 gene.  Transgenic animals expressing human minK and
CC   KVQLT1 can be used to test therapeutic agents against LQT.
XX
SQ   Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;


  Query Match             3.0%;  Score 96;  DB 18;  Length 2821;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-34;
  Matches   96;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     407 ggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccggtgttgg 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTTGG 62

Qy     467 cgcgcacccacgtccagggccgcgtctacaacttcc 502
           |||||||||||||||||||||||||||||||||||
Db      61 CGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCC 26
```

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RESULT 11
AAT90730/c
ID   AAT90730 standard; cDNA; 2821 BP.
XX
AC   AAT90730;
XX
DT   12-FEB-1998  (first entry)
XX
DE   Human KVLQT1 full-length cDNA.
XX
KW   KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW   diagnosis; therapy; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             88..1833
FT                   /*tag=  a
XX
PN   WO9723598-A2.
XX
PD   03-JUL-1997.
XX
PF   20-DEC-1996;   96WO-US19756.
XX
PR   29-OCT-1996;   96US-0739383.
PR   22-DEC-1995;   95US-0019014.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Curran ME,  Keating MT,  Sanguinetti MC;
XX
DR   WPI; 1997-402190/37.
DR   P-PSDB; AAW30038.
XX
PT   Human minK and Xenopus KVLQT1 coding sequences - used for assays for
PT   identifying drugs which can be used for preventing or treating long
PT   QT syndrome
XX
PS   Example 9; Page 76-79; 105pp; English.
XX
CC   This cDNA sequence inoludes a full-length coding sequence for human
CC   KVLQT1 (see AAW30038), a novel cardiac potassium channel protein.
CC   The sequence was assembled from partial clones isolated from human
CC   pancreatic and cardiac cDNA libraries.  KVLQT1 was mapped to
CC   chromosome 11p15.5 making it a candidate for the long QT syndrome
CC   (LQT) gene.  LQT is an inherited cardiac arrhythmia.  One intragenic
CC   deletion and 10 different missense mutations which cause LQT have
CC   been identified in KVLQT1.  The KVLQT1 gene product coassembles
CC   with human minK to form a cardiac IKs potassium channel.
CC   Coexpression of these 2 proteins in a host cell provides a means
CC   for screening for drugs useful in treating or preventing LQT.  The
CC   products can also be used for studying mechanisms underlying common
CC   arrhythmias and for presymptomatic diagnosis of LQT.  Transgenic
CC   animals expressing human minK and KVQLT1 can be used to test
CC   therapeutic agents against LQT.
XX
SQ   Sequence 2821 BP; 562 A; 892 C; 843 G; 524 T; 0 other;

  Query Match             3.0%;  Score 96;  DB 18;  Length 2821;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-34;
  Matches   96;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     407 ggccgccggtgagcctagacccgcgcgtctccatctacagcacgcgccgcccggtgttgg 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCATCTACAGCACGCGCCGCCCGGTGTTGG 62

Qy     467 cgcgcacccacgtccagggccgcgtctacaacttcc 502
           ||||||||||||||||||||||||||||||||||
Db      61 CGCGCACCCACGTCCAGGGCCGCGTCTACAACTTCC 26
```

```
RESULT 12
AAZ11946
ID   AAZ11946 standard; DNA; 45 BP.
XX
AC   AAZ11946;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel pore domain DNA sequence 6.
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US03826.
XX
PR   19-JAN-1999;   99US-0116448.
PR   25-FEB-1998;   98US-0076687.
PR   07-AUG-1998;   98US-0095836.
XX
PA   (AXYS ) AXYS PHARM INC.
XX
PI   Curran ME,  Hu P,  Miller AP,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel
PT   proteins, useful for the diagnosis and treatment of episodic ataxia
PT   with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS   Example 1; Page 31; 112pp; English.
XX
CC   This sequence represents a DNA encoding a pore domain from a
CC   human potassium channel and was used in the identification and
CC   isolation of human K+Hnov cDNAs (AAZ11897-Z11915). K+Hnov proteins
CC   have a high degree of homology to known potassium channels and
CC   may be alpha subunits, which form the functional channel, or
CC   accessory subunits that act to modulate the channel activity. K+Hnov
CC   cDNAs were isolated by extension of expressed sequence tags (ESTs) which
CC   were related but not identical to known human potassium channels.
CC   Potential polymorphisms detected as sequence variants between multiple
CC   independent clones. Potassium channels have critical roles in various
CC   cell types and biochemical pathways. Defective potassium channels are
CC   known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS)
CC   disorders. Nucleotides encoding K+Hnov proteins may be used for
CC   identifying homologous or related proteins and the DNA sequences encoding
CC   them. They may be used to produce compositions that modulate the
CC   expression and function of the K+Hnov protein and in studying the
CC   biochemical pathways associated with it. They may also be used for the
CC   recombinant production of K+Hnov protein in fermentation cultures.
CC   Additionally, such nucleotides may be used in gene therapy protocols for
CC   the treatment of diseases associated with abnormal potassium channels.
XX
SQ   Sequence 45 BP; 9 A; 10 C; 18 G; 8 T; 0 other;

  Query Match             1.4%;  Score 45;  DB 20;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-10;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1072 tggtgggggtggtcacagtcaccaccatcggctatggggacaag 1116
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                  ||||||||||||||||||||||||||||||||||||||||||||
Db      1 tggtgggggtggtcacagtcaccaccatcggctatggggacaag 45


RESULT  13
AAT26420
ID   AAT26420 standard; cDNA to mRNA; 83 BP.
XX
AC   AAT26420;
XX
DT   06-DEC-1996  (first entry)
XX
DE   Human gene signature HUMGS08661.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Claim 1; Page 2080; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in AAT19001-T26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC   sequences were obtained from 3'-directed cDNA libraries prepared
CC   from various human tissues; synthesis of cDNA was initiated from the
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 83 BP; 25 A; 10 C; 16 G; 31 T; 1 other;


  Query Match             1.3%;  Score 41;  DB 16;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   3101 gatctgtgttttaatgagtttcacagtgtgattttgattat 3141
           |||||||||||||||||||||||||||||||||||||||||
Db      1 gatctgtgttttaatgagtttcacagtgtgattttgattat 41


RESULT  14
AAC89984/c
ID   AAC89984 standard; cDNA; 2734 BP.
XX
AC   AAC89984;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Mutant human KVLQT1 coding sequence #1.
XX
KW   Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW   cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW   chromosome 11p15.5; long QT syndrome; ss.
XX
OS   Homo sapiens.
XX
PN   US6150104-A.
XX
PD   21-NOV-2000.
XX
PF   17-AUG-1998;   98US-0135021.
XX
PR   29-JUL-1998;   98US-0094477.
PR   13-JUN-1997;   97US-0874655.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Splawski I;
XX
DR   WPI; 2001-060013/07.
DR   P-PSDB; AAB49499.
XX
PT   DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT   syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT   or diagnosing or prognosing JLN -
XX
PS   Claim 2; Columns 91-96; 58pp; English.
XX
CC   KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC   cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
CC   chromosome 11p15.5. The present sequence is a mutant KVLQT1 coding
CC   sequence. The mutant KVLQT1 coding sequence is useful in the diagnosis of
CC   long QT syndrome and in screening humans for the presence of KVLQT1 gene
CC   variants which cause JLN syndrome.
XX
SQ   Sequence 2734 BP; 551 A; 864 C; 809 G; 510 T; 0 other;


  Query Match             1.1%;  Score 34;  DB 22;  Length 2734;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-06;
  Matches   34;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    407 ggccgccggtgagcctagacccgcgcgtctccat 440
          ||||||||||||||||||||||||||||||||||
Db     34 GGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCAT 1


RESULT  15
AAT91065
ID   AAT91065 standard; DNA; 22 BP.
XX
AC   AAT91065;
XX
DT   01-MAR-1998  (first entry)
XX
DE   Human KVLQT1 S2-S3 region PCR primer 1.
XX
KW   KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW   diagnosis; therapy; human; PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9723632-A1.
XX
PD   03-JUL-1997.
```

XX
PF 20-DEC-1996; 96WO-US19917.
XX
PR 29-OCT-1996; 96US-0739383.
PR 22-DEC-1995; 95US-0019014.
XX
PA (GENZ ) GENZYME GENETICS.
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Connors TD, Curran ME, Keating MF, Landes GM;
XX
DR WPI; 1997-402191/37.
XX
PT New isolated human potassium channel gene, KVLQT1, - used to develop
PT products for diagnosis, prevention and therapy of long QT syndrome
XX
PS Example 12; Page 44; 117pp; English.
XX
CC PCR primer 1 (AAT91065) and primer 2 (AAT91066) were designed to
CC amplify DNA encoding the S2-S3 region of human KVLQT1 (see AAW33355).
CC PCR primers (AAT91065-76) were used in single-strand conformation
CC analysis (SSCP) to define mutations in the human KVLQT1 gene (see
CC AAT94004) associated with long QT syndrome (LQT). An initial SSCP
CC identified an anomalous conformer in LQT-affected members of 6 large
CC families. Further SSCP analyses identified a KVLQT1 intragenic
CC deletion and 9 missense mutations associated with LQT in small
CC families and sporadic cases.
XX
SQ Sequence 22 BP; 2 A; 3 C; 9 G; 8 T; 0 other;

Query Match 0.7%; Score 22; DB 18; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 640 gagatcgtgctggtggtgttct 661
||||||||||||||||||||||
Db 1 gagatcgtgctggtggtgttct 22

Search completed: November 2, 2001, 13:36:12
Job time: 5048 sec

GenCore version 4.5


OM protein - protein search, using sw model

Run on: November 2, 2001, 12:02:03 ; Search time 50.72 Seconds
(without alignments)
564.701 Million cell updates/sec

Title: US-09-135-010A-113
Perfect score: 376
Sequence: 1 MNENAINSLYEAIPLPQDGS.....TWKIYIRKQSRNHHIMSPSP 376

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 4

Total number of hits satisfying chosen parameters: 138272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 38 | 10.1 | 645 | 2 | T27186 | hypothetical prote |
| 2 | 21 | 5.6 | 744 | 2 | T34116 | voltage-gated pota |
| 3 | 19 | 5.1 | 393 | 2 | JC5275 | voltage-gated pota |
| 4 | 10 | 2.7 | 528 | 2 | D65214 | hypothetical 60.8 |
| 5 | 10 | 2.7 | 528 | 2 | G86099 | hypothetical prote |
| 6 | 8 | 2.1 | 117 | 2 | B86862 | hypothetical prote |
| 7 | 8 | 2.1 | 246 | 2 | H82553 | 3-demethylubiquino |
| 8 | 8 | 2.1 | 280 | 2 | C82490 | probable potassium |
| 9 | 8 | 2.1 | 565 | 2 | D72222 | conserved hypothet |
| 10 | 7 | 1.9 | 55 | 2 | S47542 | pregnancy-specific |
| 11 | 7 | 1.9 | 90 | 2 | S24248 | Ig heavy chain V r |
| 12 | 7 | 1.9 | 109 | 2 | S24254 | Ig heavy chain V r |
| 13 | 7 | 1.9 | 109 | 2 | S24253 | Ig heavy chain V r |
| 14 | 7 | 1.9 | 110 | 2 | S24250 | Ig heavy chain V r |
| 15 | 7 | 1.9 | 113 | 2 | S24247 | Ig heavy chain V r |
| 16 | 7 | 1.9 | 114 | 2 | S75337 | hypothetical prote |
| 17 | 7 | 1.9 | 116 | 2 | S75339 | hypothetical prote |
| 18 | 7 | 1.9 | 119 | 2 | T08728 | NADH dehydrogenase |
| 19 | 7 | 1.9 | 164 | 2 | T11377 | NADH dehydrogenase |
| 20 | 7 | 1.9 | 176 | 2 | T23935 | hypothetical prote |
| 21 | 7 | 1.9 | 184 | 2 | T00277 | conserved hypothet |
| 22 | 7 | 1.9 | 193 | 2 | S37045 | transposase - Pseu |
| 23 | 7 | 1.9 | 241 | 2 | D64511 | hypothetical prote |
| 24 | 7 | 1.9 | 244 | 2 | I40362 | H+-transporting AT |
| 25 | 7 | 1.9 | 244 | 2 | F69260 | nitrate ABC transp |
| 26 | 7 | 1.9 | 256 | 1 | QQOMC2 | B256 protein - cas |
| 27 | 7 | 1.9 | 261 | 1 | QBBPL | recombination prot |
| 28 | 7 | 1.9 | 261 | 2 | H85637 | hypothetical prote |
| 29 | 7 | 1.9 | 261 | 2 | E85848 | hypothetical prote |
| 30 | 7 | 1.9 | 268 | 2 | D64223 | probable 1-acylgly |
| 31 | 7 | 1.9 | 299 | 2 | T20605 | hypothetical prote |
| 32 | 7 | 1.9 | 307 | 2 | H82743 | methionyl-tRNA for |
| 33 | 7 | 1.9 | 332 | 2 | C64164 | thiamin-binding pe |
| 34 | 7 | 1.9 | 335 | 2 | S44635 | f22b7.7 protein - |
| 35 | 7 | 1.9 | 338 | 2 | F69437 | hypothetical prote |
| 36 | 7 | 1.9 | 344 | 2 | T18019 | probable site-spec |
| 37 | 7 | 1.9 | 355 | 2 | A72331 | transcription regu |
| 38 | 7 | 1.9 | 357 | 2 | T27334 | hypothetical prote |
| 39 | 7 | 1.9 | 376 | 2 | S57867 | oncogene 1 - human |
| 40 | 7 | 1.9 | 387 | 2 | H65132 | hypothetical 44.3 |
| 41 | 7 | 1.9 | 395 | 1 | G69594 | cytochrome P450 bi |
| 42 | 7 | 1.9 | 405 | 2 | T21188 | hypothetical prote |
| 43 | 7 | 1.9 | 417 | 2 | H83708 | hypothetical prote |
| 44 | 7 | 1.9 | 436 | 2 | T03702 | hypothetical prote |
| 45 | 7 | 1.9 | 444 | 2 | T26229 | hypothetical prote |

ALIGNMENTS

RESULT 1
T27186
hypothetical protein Y54G9A.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27186
R;Smye, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20324
A;Accession: T27186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-645 <WIL>
A;Cross-references: EMBL:AL032648; PIDN:CAA21699.1; GSPDB:GN00020; CESP:Y54G9A.3
A;Experimental source: clone Y54G9A
C;Genetics:
A;Gene: CESP:Y54G9A.3
A;Map position: 2
A;Introns: 56/3; 100/2; 148/1; 411/2; 541/2; 575/3

Query Match 10.1%; Score 38; DB 2; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.1e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 RLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLAEKD 252
||||||||||||||||||||||||||||||||||||||||
Db 227 RLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLAEKD 264

RESULT 2
T34116
voltage-gated potassium channel klq-1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T34116
R;Wilcox, L.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid C25B8.
A;Reference number: Z21479
A;Accession: T34116
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-744 <WIL>
A;Cross-references: EMBL:U41556; PIDN:AAC70874.1; GSPDB:GN00028; CESP:C25B8.1
A;Experimental source: strain Bristol N2; clone C25B8
C;Genetics:
A;Gene: klq-1; CESP:C25B8.1
A;Map position: X
A;Introns: 31/3; 64/1; 81/3; 131/2; 161/3; 204/1; 262/3; 304/3; 341/3; 402/2; 426/1;

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  Query Match             5.6%;  Score 21;  DB 2;  Length 744;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     303 ISFFALPAGILGSGFALKVQQ 323
           |||||||||||||||||||||
Db     334 ISFFALPAGILGSGFALKVQQ 354


RESULT   3
JC5275
voltage-gated potassium channel protein - human
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 05-Nov-1999
C;Accession: JC5275
R;Yokoyama, M.; Nishi, Y.; Yoshii, J.; Okubo, K.; Matsubara, K.
DNA Res. 3, 311-320, 1996
A;Title: Identification and cloning of neuroblastoma-specific and nerve tissue-specific
A;Reference number: JC5272; MUID:97191543
A;Contents: neuroblastma cell
A;Accession: JC5275
A;Molecule type: mRNA
A;Residues: 1-393 <YQK>
A;Cross-references: DDBJ:D82346; NID:g1841341; PIDN:BAA11557.1; PID:d1012224; PID:g18413

  Query Match             5.1%;  Score 19;  DB 2;  Length 393;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-11;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     304 SFFALPAGILGSGFALKVQ 322
           ||||||||||||||||||||
Db     303 SFFALPAGILGSGFALKVQ 321


RESULT   4
D65214
hypothetical 60.8 kD protein in ssb-soxs intergenic region - Escherichia coli (strain K-
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 29-Sep-1999
C;Accession: D65214
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D65214
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-528 <BLAT>
A;Cross-references: GB:AE000479; GB:U00096; NID:g2367340; PIDN:AAC77031.1; PID:g1790496;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: yjcC
C;Superfamily: probable membrane protein ylaB

  Query Match             2.7%;  Score 10;  DB 2;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     306 FALPAGILGS 315
           ||||||||||
Db     245 FALPAGILGS 254


RESULT   5
G86099
hypothetical protein yjcC [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C;Accession: G86099
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G86099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-528 <STO>
A;Cross-references: GB:AE005174; NID:g12519015; PIDN:AAG59259.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yjcC

  Query Match             2.7%;  Score 10;  DB 2;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     306 FALPAGILGS 315
           ||||||||||
Db     245 FALPAGILGS 254


RESULT   6
B86862
hypothetical protein ytgE [imported] - Lactococcus lactis subsp. lactis (strain IL140
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C;Accession: B86862
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. in press, 2001
A;Title: The complete genome sequence of the lactic acid bacterium.
A;Reference number: A86625
A;Accession: B86862
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <STO>
A;Cross-references: GB:AE005176; NID:g12724933; PIDN:AAK05996.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ytgE

  Query Match             2.1%;  Score 8;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 2.2;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      35 ELKRETLV 42
           ||||||||
Db      66 ELKRETLV 73


RESULT   7
H82553
3-demethylubiquinone-9 3-methyltransferase XF2471 [imported] - Xylella fastidiosa (st
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: H82553
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82553
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-246 <SIM>
A;Cross-references: GB:AE004055; GB:AE003849; NID:g9107661; PIDN:AAF85269.1; GSPDB:GN
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
```

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2471
C;Superfamily: 3-demethylubiquinone-9 3-O-methyltransferase; bioC homology

Query Match 2.1%; Score 8; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 134 GAEYVVRL 141
||||||||
Db 172 GAEYVVRL 179

RESULT 8
C82490
probable potassium channel protein VCA0194 [imported] - Vibrio cholerae (strain N16961 s
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: C82490
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833
A;Accession: C82490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-280 <HEI>
A;Cross-references: GB:AE004359; GB:AE003853; NID:g9657575; PIDN:AAF96107.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0194
A;Map position: 2

Query Match 2.1%; Score 8; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 264 SYADALWW 271
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Db 151 SYADALWW 158

RESULT 9
D72222
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72222
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316
A;Accession: D72222
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <ARN>
A;Cross-references: GB:AE001809; GB:AE000512; NID:g4982257; PIDN:AAD36749.1; PID:g498225
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1682

Query Match 2.1%; Score 8; DB 2; Length 565;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 349 AAENPDSA 356
||||||||
Db 133 AAENPDSA 140

RESULT 10
S47542
pregnancy-specific beta(1)-glycoprotein-11 - human
C;Species: Homo sapiens (man)
C;Date: 26-Dec-1994 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S47542
R;Joe, T.W.; McLenachan, P.A.; Mansfield, B.C.
Biochim. Biophys. Acta 1219, 195-197, 1994
A;Title: Sequence of a novel pregnancy-specific beta(1)-glycoprotein C-terminal domai
A;Reference number: S47542; MUID:94368856
A;Accession: S47542
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-55 <JOE>
A;Cross-references: EMBL:L17043
A;Note: 33-X is the translation of a stop-codon; spliced according to feature informa
C;Genetics:
A;Introns: 11/2; 19/1; 33/3; 39/2; 43/1
C;Keywords: glycoprotein

Query Match 1.9%; Score 7; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 PISVIDL 169
|||||||
Db 41 PISVIDL 47

RESULT 11
S24248
Ig heavy chain V region (VH26) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S24248
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B
A;Reference number: S24247
A;Accession: S24248
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <STE>
A;Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA47454.1; PID:g38396
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 1.9%; Score 7; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VGVWGRL 157
|||||||
Db 4 VGVWGRL 10

RESULT 12

S24254
Ig heavy chain V region (VH26-DXP2-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24254
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel
A;Reference number: S24247
A;Accession: S24254
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <STE>
A;Cross-references: EMBL:X67062
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 1.9%; Score 7; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VGVWGRL 157
||||||| 
Db 4 VGVWGRL 10

RESULT 13
S24253
Ig heavy chain V region (VH26-DLR4-JH6) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24253
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel
A;Reference number: S24247
A;Accession: S24253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <STE>
A;Cross-references: EMBL:X67061
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-94/Domain: immunoglobulin homology <IMM>

Query Match 1.9%; Score 7; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VGVWGRL 157
||||||| 
Db 1 VGVWGRL 7

RESULT 14
S24250
Ig heavy chain V region (VH26-DN1-JH4) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24250
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel
A;Reference number: S24247
A;Accession: S24250
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <STE>
A;Cross-references: EMBL:X67071
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 1.9%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VGVWGRL 157
||||||| 
Db 4 VGVWGRL 10

RESULT 15
S24247
Ig heavy chain V region (VH26-DLR2-JH3) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24247
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B
A;Reference number: S24247
A;Accession: S24247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <STE>
A;Cross-references: EMBL:X67060; NID:g38377; PIDN:CAA47445.1; PID:g38378
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 1.9%; Score 7; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 151 VGVWGRL 157
||||||| 
Db 4 VGVWGRL 10

Search completed: November 2, 2001, 12:03:05
Job time: 62 sec

GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: November 2, 2001, 12:11:29 ; Search time 101.36 Seconds
(without alignments)
5941.187 Million cell updates/sec

Title: US-09-135-010A-1
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 324599 seqs, 94655562 residues

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Total number of hits satisfying chosen parameters: 34250

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| | 35 | 18 | 0.6 | 1656 | 6 | 5449756-9 | Patent No. 5449756 |
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ALIGNMENTS

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; Sequence 1, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
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;   ORGANISM: Homo sapiens
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;   NAME/KEY: CDS
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US-09-135-021-5
; Sequence 5, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 3182
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (163)..(1011)
;   FEATURE:
;   NAME/KEY: mutation
;   LOCATION: (730)
;   OTHER INFORMATION: This base is an insertion as compared to the
;   OTHER INFORMATION: wild-type.
US-09-135-021-5

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3181;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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; Sequence 79, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
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Qy   1200 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    753 tcttggctcggggtttgccctgaaggtgcagcagaagcagaggcagaagcacttcaaccg 812

Qy   1260 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    813 gcagatcccggcggcagcctcactcattcagaccgcatggaggtgctatgctgccgagaa 872

Qy   1320 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    873 ccccgactcctccacctggaagatctacatccggaaggccccccggagccacactctgct 932

Qy   1380 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    933 gtcacccagccccaaacccaagaagtctgtggtggtaaagaaaaaaaagttcaagctgga 992

Qy   1440 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    993 caaagacaatggggtgactcctggagagaagatgctcacagtcccccatatcacgtgcga 1052

Qy   1500 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1053 ccccccagaagagcggcggctggaccacttctctgtcgacggctatgacagttctgtaag 1112

Qy   1560 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1113 gaagagcccaacactgctggaagtgagcatgccccatttcatgagaaccaacagcttcgc 1172

Qy   1620 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1173 cgaggacctggacctggaaggggagactctgctgacacccatcacccacatctcacagct 1232

Qy   1680 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1233 gcgggaacaccatcgggccaccattaaggtcattcgacgcatgcagtactttgtggccaa 1292

Qy   1740 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1799
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1293 gaagaaattccagcaagcgcggaagccttacgatgtgcgggacgtcattgagcagtactc 1352

Qy   1800 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1859
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1353 gcagggccacctcaacctcatggtgcgcatcaaggagctgcagaggaggctggaccagtc 1412

Qy   1860 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1919
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1413 cattgggaagccctcactgttcatctccgtctcagaaaagagcaaggatcgcggcagcaa 1472

Qy   1920 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1979
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1473 cacgatcggcgcccgcctgaaccgagtagaagacaaggtgacgcagctggaccagaggct 1532
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Qy   1980 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 2039
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1533 ggcactcatcaccgacatgcttcaccagctgctctccttgcacggtggcagcacccccgg 1592

Qy   2040 cagcggcggccccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 2099
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1593 cagcggcggccccccccagagagggcggggcccacatcacccagccctgcggcagtggcgg 1652

Qy   2100 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 2159
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1653 ctccgtcgaccctgagctcttcctgcccagcaacaccctgcccacctacgagcagctgac 1712

Qy   2160 cgtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggc 2219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1713 cgtgcccaggaggggccccgatgaggggtcctgaggaggggatggggctgggggatgggc 1772

Qy   2220 ctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctc 2279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1773 ctgagtgagaggggaggccaagagtggccccacctggccctctctgaaggaggccacctc 1832

Qy   2280 ctaaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgc 2339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1833 ctaaaaggcccagagagaagagccccactctcagaggccccaataccccatggaccatgc 1892

Qy   2340 tgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtggg 2399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1893 tgtctggcacagcctgcacttgggggctcagcaaggccacctcttcctggccggtgtggg 1952

Qy   2400 ggccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttg 2459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1953 ggccccgtctcaggtctgagttgttaccccaagcgccctggcccccacatggtgatgttg 2012

Qy   2460 acatcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatgg 2519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2013 acatcactggcatggtggttgggacccagtggcagggcacagggcctggcccatgtatgg 2072

Qy   2520 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccagggggcttcctgag 2579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2073 ccaggaagtagcacaggctgagtgcaggcccaccctgcttggcccagggggcttcctgag 2132

Qy   2580 gggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggca 2639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2133 gggagacagagcaacccctggaccccagcctcaaatccaggaccctgccaggcacaggca 2192

Qy   2640 gggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatt 2699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2193 gggcaggaccagcccacgctgactacagggccaccggcaataaaagcccaggagcccatt 2252

Qy   2700 tggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagact 2759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2253 tggagggcctgggcctggctccctcactctcaggaaatgctgacccatgggcaggagact 2312

Qy   2760 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccca 2819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2313 gtggagactgctcctgagcccccagcttccagcaggagggacagtctcaccatttccccca 2372

Qy   2820 gggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcct 2879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2373 gggcacgtggttgagtgggggggaacgcccacttccctgggttagactgccagctcttcct 2432

Qy   2880 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2939
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2433 agctggagaggagccctgcctctccgcccctgagcccactgtgcgtggggctcccgcctc 2492

Qy   2940 caaccccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2493 caaccccctcgcccagtcccagcagccagccaaacacacagaaggggactgccacctcccc 2552

Qy   3000 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2553 ttgccagctgctgagccgcagagaagtgacggttcctacacaggacaggggttccttctg 2612
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Qy   3060 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2613 ggcattacatcgcatagaaatcaataatttgtggtgatttggatctgtgttttaatgagt 2672

Qy   3120 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2673 ttcacagtgtgattttgattattaattgtgcaagcttttcctaataaacgtggagaatca 2732

Qy   3180 ca 3181
          ||
Db   2733 ca 2734
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RESULT 4
US-09-135-021-79/c
; Sequence 79, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 2734
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1743)
US-09-135-021-79

Query Match 1.1%; Score 34; DB 3; Length 2734;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    407 ggccgccggtgagcctagacccgcgcgtctccat 440
          ||||||||||||||||||||||||||||||||||
Db     34 GGCCGCCGGTGAGCCTAGACCCGCGCGTCTCCAT 1
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RESULT 5
US-09-179-558-64
; Sequence 64, Application US/09179558
; Patent No. 6180612
; GENERAL INFORMATION:
; APPLICANT: Hockensmith, Joel W.
; APPLICANT: Muthuswami, Rohini
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TARGETING DNA METABOLIC PROCESSES USING
; TITLE OF INVENTION: AMINOGLYCOSIDE DERIVATIVES
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/179,558
;      FILING DATE:  27-OCT-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 09/060,470
;      FILING DATE:  15-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 60/063,898
;      FILING DATE:  31-OCT-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  9426-005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)7909090
;      TELEFAX:  (212)8699741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  892 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other
US-09-179-558-64


  Query Match             0.6%;  Score 20;  DB 4;  Length 892;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     974 tgggcctcatcttctcctcg 993
           ||||||||||||||||||||
Db     610 TGGGCCTCATCTTCTCCTCG 629


RESULT   6
US-09-179-558-62
; Sequence 62, Application US/09179558
; Patent No. 6180612
;  GENERAL INFORMATION:
;    APPLICANT:  Hockensmith, Joel W.
;    APPLICANT:  Muthuswami, Rohini
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR
;    TITLE OF INVENTION:  TARGETING DNA METABOLIC PROCESSES USING
;    TITLE OF INVENTION:  AMINOGLYCOSIDE DERIVATIVES
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PENNIE & EDMONDS LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/179,558
;      FILING DATE:  27-OCT-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 09/060,470
;      FILING DATE:  15-APR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 60/063,898
;      FILING DATE:  31-OCT-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  9426-005-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)7909090
;      TELEFAX:  (212)8699741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  62:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  936 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other
US-09-179-558-62


  Query Match             0.6%;  Score 20;  DB 4;  Length 936;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     974 tgggcctcatcttctcctcg 993
           ||||||||||||||||||||
Db     654 TGGGCCTCATCTTCTCCTCG 673


RESULT   7
US-08-968-751-1/c
; Sequence 1, Application US/08968751
; Patent No. 5948643
;  GENERAL INFORMATION:
;    APPLICANT:  Rubinfeld, Bonnee
;    APPLICANT:  Polakis, Paul G.
;    APPLICANT:  Ligenfelter, Carol
;    APPLICANT:  Vuong, Terilyn T.
;    TITLE OF INVENTION:  MODULATORS OF BRCA1 ACTIVITY
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ONYX Pharmaceuticals, Inc.
;      STREET:  3031 Research Drive
;      CITY:  Richmond
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94806
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/968,751
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giotta, Gregory
;      REGISTRATION NUMBER:  32,028
;      REFERENCE/DOCKET NUMBER:  ONYX1024 GG
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 262-8710
;      TELEFAX:  (510) 222-9758
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2065 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  103..1512
US-08-968-751-1
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Query Match 0.6%; Score 20; DB 2; Length 2065;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2548 cccaccctgcttggcccagg 2567
||||||||||||||||||||
Db 1939 CCCACCCTGCTTGGCCCAGG 1920

RESULT 8
US-09-135-021-39
; Sequence 39, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-021-39

Query Match 0.6%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 99 ctcgccttcgctgcagctc 117
|||||||||||||||||||
Db 1 ctcgccttcgctgcagctc 19

RESULT 9
US-09-135-021-40/c
; Sequence 40, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-021-40

Query Match 0.6%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 414 ggtgagcctagacccgcgc 432
|||||||||||||||||||
Db 19 GGTGAGCCTAGACCCGCGC 1

RESULT 10
US-08-306-691B-42/c
; Sequence 42, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7011 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-306-691B-42

Query Match 0.6%; Score 19; DB 1; Length 7011;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2346 gcacagcctgcacttgggg 2364
|||||||||||||||||||
Db 3821 GCACAGCCTGCACTTGGGG 3803

RESULT 11
US-09-135-021-41
; Sequence 41, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
; TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
; FILE REFERENCE: 2323-128
; CURRENT APPLICATION NUMBER: US/09/135,021A
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/874,655
; EARLIER FILING DATE: 1997-06-13

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;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-135-021-41


  Query Match             0.6%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    372 cgccgcgcccccagttgc 389
          ||||||||||||||||||
Db      1 cgccgcgcccccagttgc 18


RESULT  12
US-09-135-021-72/c
; Sequence 72, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-135-021-72


  Query Match             0.6%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   2200 gatggggctgggggatgg 2217
          ||||||||||||||||||
Db     18 GATGGGGCTGGGGGATGG 1


RESULT  13
US-09-135-021-73
; Sequence 73, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(18)
US-09-135-021-73


  Query Match             0.6%;  Score 18;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 60;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    721 ctctgggggcggctgcgc 738
          ||||||||||||||||||
Db      1 ctctgggggcggctgcgc 18


RESULT  14
US-08-519-777-30/c
; Sequence 30, Application US/08519777
; Patent No. 5739307
;  GENERAL INFORMATION:
;    APPLICANT:  JOHNSON JR., EUGENE M.
;    APPLICANT:  MILBRANDT, JEFFREY D.
;    APPLICANT:  KOTZBAUER, PAUL T.
;    APPLICANT:  LAMPE, PATRICIA A.
;    TITLE OF INVENTION:  NEURTURIN AND RELATED GROWTH FACTORS
;    NUMBER OF SEQUENCES:  78
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROGERS, HOWELL & HAFERKAMP, L.C.
;      STREET:  7733 FORSYTH BOULEVARD, SUITE 1400
;      CITY:  ST. LOUIS
;      STATE:  MISSOURI
;      COUNTRY:  US
;      ZIP:  63105-1817
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/519,777
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  HOLLAND, DONALD R.
;      REGISTRATION NUMBER:  35,197
;      REFERENCE/DOCKET NUMBER:  953095
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314) 727-5188
;      TELEFAX:  (314) 727-6092
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  419 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-519-777-30


  Query Match             0.6%;  Score 18;  DB 1;  Length 419;
  Best Local Similarity   100.0%;  Pred. No. 54;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    359 ccccggccgcgcccgccg 376
          ||||||||||||||||||
Db    122 CCCCGGCCGCGCCCGCCG 105


RESULT  15
US-08-742-035-30/c
```

; Sequence 30, Application US/08742035
; Patent No. 5747655
; GENERAL INFORMATION:
; APPLICANT: JOHNSON JR., EUGENE M.
; APPLICANT: MILBRANDT, JEFFREY D.
; APPLICANT: KOTZBAUER, PAUL T.
; APPLICANT: LAMPE, PATRICIA A.
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: US
; ZIP: 63105-1817
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,035
; FILING DATE: 01-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/519,777
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 953095
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-742-035-30

Query Match 0.6%; Score 18; DB 1; Length 419;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 359 ccccggccgcgcccgccg 376
||||||||||||||||||
Db 122 CCCCGGCCGCGCCCGCCG 105

Search completed: November 2, 2001, 13:30:48
Job time: 4759 sec

Job time: 8495 sec

```
PS   Disclosure; Fig 2; 30pp; German.
XX
CC   This invention describes a novel eukaryotic expression vector (A)
CC   comprising a nucleic acid sequence (I), encoding a potassium channel
CC   subunit (II), arranged so that it can be functionally expressed in
CC   eukaryotes. (A) are used to express bacterial potassium channels in
CC   eukaryotes, specifically for screening compounds for their ability to
CC   open, close or (in)activate the channels or to alter their biophysical
CC   properties, especially to identify potential antibiotics.
XX
SQ   Sequence   21 AA;


  Query Match             5.6%;  Score 21;  DB 21;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-13;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    266 ADALWWGVVTVTTIGYGDKVP 286
          |||||||||||||||||||||
Db      1 adalwwgvvtvttigygdkvp 21


RESULT  14
AAB49495
ID   AAB49495 standard; Protein; 283 AA.
XX
AC   AAB49495;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Mutant human KVLQT1 #2.
XX
KW   Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW   cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW   chromosome 11p15.5; long QT syndrome.
XX
OS   Homo sapiens.
XX
PN   US6150104-A.
XX
PD   21-NOV-2000.
XX
PF   17-AUG-1998;   98US-0135021.
XX
PR   29-JUL-1998;   98US-0094477.
PR   13-JUN-1997;   97US-0874655.
XX
PA   (UTAH-)-UNIV UTAH RES FOUND.
XX
PI   Keating MT, Splawski I;
XX
DR   WPI; 2001-060013/07.
DR   N-PSDB; AAC89914.
XX
PT   DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT   syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT   or diagnosing or prognosing JLN -
XX
PS   Example 4; Columns 67-70; 58pp; English.
XX
CC   KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC   cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
CC   chromosome 11p15.5. The present sequence is a mutant KVLQT1. The coding
CC   sequence for the present protein is useful in the diagnosis of long QT
CC   syndrome and in screening humans for the presence of KVLQT1 gene variants
CC   which cause JLN syndrome.
XX
SQ   Sequence   283 AA;


  Query Match             5.6%;  Score 21;  DB 22;  Length 283;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     73 QGRVYNFLERPTGWKCFVYHF 93
          |||||||||||||||||||||
Db    107 qgrvynflerptgwkcfvyhf 127


RESULT  15
AAY08342
ID   AAY08342 standard; Protein; 807 AA.
XX
AC   AAY08342;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Human nKTQ1 protein.
XX
KW   KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW   benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
KW   JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
KW   detection; gene therapy; drug screening; nKTQ1.
XX
OS   Homo sapiens.
XX
PN   WO9921875-A1.
XX
PD   06-MAY-1999.
XX
PF   23-OCT-1998;   98WO-US22375.
XX
PR   24-OCT-1997;   97US-0063147.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Charlier C,  Leppert MF,  Singh NA;
XX
DR   WPI; 1999-312938/26.
XX
PT   Nucleic acid encoding potassium channels KCNQ2 and 3
XX
PS   Disclosure; Page 125-128; 195pp; English.
XX
CC   This invention describes novel human and mouse potassium channel proteins
CC   KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC   KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC   prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC   epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC   that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC   in cell-free form) are used to screen for agents that can be used to
CC   treat or prevent these forms of epilepsy. Fragments of the encoding
CC   nucleic acids are used as probes or primers, either for detecting
CC   mutations or for isolation of related sequences, while the complete
CC   sequences may be used in gene therapy to provide wild-type protein.
CC   Antibodies specific for mutant or wild-type proteins are used as
CC   diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC   useful in rational design of drugs and therapeutically (in replacement
CC   therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC   3 sequences can now be diagnosed early (before symptoms are manifest),
CC   and better treatment options will be available.
XX
SQ   Sequence   807 AA;


  Query Match             5.6%;  Score 21;  DB 20;  Length 807;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-12;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    303 ISFFALPAGILGSGFALKVQQ 323
          |||||||||||||||||||||
Db    333 isffalpagilgsgfalkvqq 353


Search completed: November  3, 2001, 13:19:10
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XX
PD   21-NOV-2000.
XX
PF   17-AUG-1998;   98US-0135021.
XX
PR   29-JUL-1998;   98US-0094477.
PR   13-JUN-1997;   97US-0874655.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Splawski I;
XX
DR   WPI; 2001-060013/07.
DR   N-PSDB; AAC89911.
XX
PT   DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT   syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT   or diagnosing or prognosing JLN -
XX
PS   Example 4; Columns 59-64; 58pp; English.
XX
CC   The present sequence is wild-type human KVLQT1. KVLQT1 is a cardiac
CC   potassium channel and mutations in the KVLQT1 gene cause Jervell and
CC   Lange-Nielsen Syndrome (JLN). KVLQT1 maps to chromosome 11p15.5. The
CC   present invention relates to a mutant KVLQT1 coding sequence (see
CC   AAC89914). The mutant KVLQT1 coding sequence is useful in the diagnosis
CC   of long QT syndrome and in screening humans for the presence of KVLQT1
CC   gene variants which cause JLN syndrome.
XX
SQ   Sequence   676 AA;

  Query Match           18.4%;  Score 69;  DB 22;  Length 676;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     219 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 278

Qy     245 FVYLAEKDA 253
           |||||||||
Db     279 fvylaekda 287


RESULT  12
AAY08343
ID   AAY08343 standard; Protein; 677 AA.
XX
AC   AAY08343;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Human KCNQ1 protein.
XX
KW   KCNQ2; KCNQ3; human; murine; potassium channel; diagnosis; prognosis;
KW   benign familial neonatal epilepsy; BFNE; juvenile myotonic epilepsy;
KW   JME; rolandic epilepsy; mutant; treatment; screening; epilepsy;
KW   detection; gene therapy; drug screening; KCNQ1.
XX
OS   Homo sapiens.
XX
PN   WO9921875-A1.
XX
PD   06-MAY-1999.
XX
PF   23-OCT-1998;   98WO-US22375.
XX
PR   24-OCT-1997;   97US-0063147.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Charlier C,  Leppert MF,  Singh NA;
XX
DR   WPI; 1999-312938/26.
XX
PT   Nucleic acid encoding potassium channels KCNQ2 and 3
XX
PS   Disclosure; Page 128-130; 195pp; English.
XX
CC   This invention describes novel human and mouse potassium channel proteins
CC   KCNQ2 and KCNQ3. Detecting mutations in sequences that encode KCNQ2 or
CC   KCNQ3, or the loss of one copy of these genes, is used for diagnosis and
CC   prognosis of benign familial neonatal epilepsy (BFNE), juvenile myotonic
CC   epilepsy (JME) or rolandic epilepsy (RE). Cells (or transgenic animals)
CC   that express wild-type or mutant KCNQ2 or 3 (also the proteins themselves
CC   in cell-free form) are used to screen for agents that can be used to
CC   treat or prevent these forms of epilepsy. Fragments of the encoding
CC   nucleic acids are used as probes or primers, either for detecting
CC   mutations or for isolation of related sequences, while the complete
CC   sequences may be used in gene therapy to provide wild-type protein.
CC   Antibodies specific for mutant or wild-type proteins are used as
CC   diagnostic reagents and for drug screening. The KCNQ2 and 3 proteins are
CC   useful in rational design of drugs and therapeutically (in replacement
CC   therapies). The forms of epilepsy associated with mutations in KCNQ2 and
CC   3 sequences can now be diagnosed early (before symptoms are manifest),
CC   and better treatment options will be available.
XX
SQ   Sequence   677 AA;

  Query Match           18.4%;  Score 69;  DB 20;  Length 677;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 279

Qy     245 FVYLAEKDA 253
           |||||||||
Db     280 fvylaekda 288


RESULT  13
AAB11385
ID   AAB11385 standard; Protein; 21 AA.
XX
AC   AAB11385;
XX
DT   22-FEB-2001  (first entry)
XX
DE   Potassium channel protein KVLQT1 P region.
XX
KW   LQT B; potassium channel protein; screening; antibiotic.
XX
OS   Unidentified.
XX
PN   EP1046708-A1.
XX
PD   25-OCT-2000.
XX
PF   13-APR-2000; 2000EP-0107916.
XX
PR   23-APR-1999;   99DE-1020044.
XX
PA   (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH.
XX
PI   Pongs O;
XX
DR   WPI; 2000-657763/64.
XX
PT   Expression vector for bacterial potassium channel that is functional in
PT   eukaryotic cells, used to screen for channel modulators and potential
PT   antibiotics -
XX
```

```
XX
AC   AAY57368;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human KVLQT1 protein.
XX
KW   KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
KW   antiarrhythmic; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO200006600-A1.
XX
PD   10-FEB-2000.
XX
PF   06-OCT-1998;   98WO-US17838.
XX
PR   29-JUL-1998;   98US-0094477.
PR   17-AUG-1998;   98US-0135020.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Sanguinetti MC,  Splawski I;
XX
DR   WPI; 2000-195262/17.
DR   N-PSDB; AAZ90669.
XX
PT   Mutant forms of genes encoding minK protein and KVLQT1 protein involved
PT   in cardiac potassium channel formation useful for screening drugs, for
PT   preventing and treating cardiac arrhythmia  -
XX
PS   Claim 37; Fig 5A-B; 167pp; English.
XX
CC   The invention relates to KVLQT1 and KCNE1 genes, associated with long
CC   QT (LQT) syndrome. It provides a minK protein comprising a mutation which
CC   substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
CC   Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening
CC   KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
CC   treating LQT. The ability to predict LQT enables physicians to prevent
CC   the diseases with medical therapy such as beta blocking agents and opts
CC   for better treatments. The present sequence represents the human
CC   KVLQT1 protein.
XX
SQ   Sequence   676 AA;


  Query Match             18.4%;  Score 69;  DB 21;  Length 676;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     219 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 278

Qy     245 FVYLAEKDA 253
           |||||||||
Db     279 fvylaekda 287


RESULT  10
AAY80562
ID   AAY80562 standard; Protein; 676 AA.
XX
AC   AAY80562;
XX
DT   06-JUN-2000  (first entry)
XX
DE   Human long QT syndrome-associated KVLQT1 protein.
XX
KW   KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1;
KW   cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy;
KW   chromosome 11p15.5.
XX
OS   Homo sapiens.
XX
PN   WO200006199-A1.
XX
PD   10-FEB-2000.
XX
PF   12-MAY-1999;   99WO-US10260.
XX
PR   29-JUL-1998;   98US-0094477.
PR   17-AUG-1998;   98US-0135010.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (GENZ ) GENZYME CORP.
XX
PI   Keating MT,  Sanguinetti MC,  Curran ME,  Landes GM,  Connors TD;
PI   Burn TC,  Splawski I;
XX
DR   WPI; 2000-195199/17.
DR   N-PSDB; AAZ98901.
XX
PT   New isolated mutant KVLQT1 nucleic acids, useful for developing
PT   products for the diagnosis, prevention and treatment of long QT
PT   syndrome  -
XX
PS   Claim 54; Fig 5A-B; 178pp; English.
XX
CC   The invention relates to KVLQT1 nucleic acids which have a mutation
CC   compared to wild-type KVLQT1. This sequence corresponds to the human
CC   wild type KVLQT1 protein. The protein forms a cardiac I(ks) potassium
CC   channel with the KCNE1 protein (AAY80563). The KVLQT1 protein contains
CC   6 putative transmembrane segments and a pore forming region. Mutations
CC   in the KVLQT1 or KCNE1 genes result in cardiac arrhythmias observed as
CC   a prolonged QT curve in electrocardiograms (Long QT syndrome). The genes
CC   and proteins can be used for the diagnosis of subjects with long QT
CC   syndrome. They can also be used to screen for drugs which can be used
CC   for treating or preventing long QT syndrome. The KVLQT1 nucleic acids
CC   can be used for gene therapy, and KVLQT1 peptides can be used for
CC   peptide therapy.
XX
SQ   Sequence   676 AA;


  Query Match             18.4%;  Score 69;  DB 21;  Length 676;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     219 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 278

Qy     245 FVYLAEKDA 253
           |||||||||
Db     279 fvylaekda 287


RESULT  11
AAB49494
ID   AAB49494 standard; Protein; 676 AA.
XX
AC   AAB49494;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Human KVLQT1.
XX
KW   Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW   cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW   chromosome 11p15.5; long QT syndrome.
XX
OS   Homo sapiens.
XX
PN   US6150104-A.
```

```
XX
DE   Human KVLQT1 associated with long QT syndrome.
XX
KW   KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW   diagnosis; therapy; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          28..49
FT                   /label= S1
FT                   /note= "transmembrane domain"
FT   Domain          53..75
FT                   /label= S2
FT                   /note= "transmembrane domain"
FT   Domain          103..121
FT                   /label= S3
FT                   /note= "transmembrane domain"
FT   Domain          126..144
FT                   /label= S4
FT                   /note= "transmembrane domain"
FT   Domain          168..187
FT                   /label= S5
FT                   /note= "transmembrane domain"
FT   Misc-difference 194
FT                   /note= "N-glycosylated"
FT   Domain          206..225
FT                   /label= Pore
FT   Domain          230..259
FT                   /label= S6
FT                   /note= "transmembrane domain"
XX
PN   WO9723598-A2.
XX
PD   03-JUL-1997.
XX
PF   20-DEC-1996;   96WO-US19756.
XX
PR   29-OCT-1996;   96US-0739383.
PR   22-DEC-1995;   95US-0019014.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Curran ME, Keating MT, Sanguinetti MC;
XX
DR   WPI; 1997-402190/37.
XX
PT   Human minK and Xenopus KVLQT1 coding sequences - used for assays for
PT   identifying drugs which can be used for preventing or treating long
PT   QT syndrome
XX
PS   Example 8; Fig 3A; 105pp; English.
XX
CC   This protein comprises a novel human cardiac potassium channel
CC   protein. It is encoded by the KVLQT1 gene (see AAT90730) that
CC   is associated with long QT syndrome (LQT) gene, an inherited
CC   cardiac arrhythmia. KVLQT1 protein coassembles with human minK
CC   to form the cardiac IKs potassium channel. IKs dysfunction is
CC   a cause of cardiac arrhythmia. Coexpression of KVLQT1 and minK
CC   in a host cell provides a means for screening for drugs useful in
CC   treating or preventing LQT. The products can also be used for
CC   studying mechanisms underlying common arrhythmias and for
CC   presymptomatic diagnosis of LQT. Transgenic animals that express
CC   human minK and KVQLT1 can be used to test therapeutic agents
CC   against LQT.
XX
SQ   Sequence   581 AA;

  Query Match             18.4%;  Score 69;  DB 18;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      124 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 183

Qy      245 FVYLAEKDA 253
            |||||||||
Db      184 fvylaekda 192


RESULT   8
AAB49499
ID   AAB49499 standard; Protein; 581 AA.
XX
AC   AAB49499;
XX
DT   08-MAR-2001  (first entry)
XX
DE   Mutant human KVLQT1 #1.
XX
KW   Human; KVLQT1; antiarrhythmic; cardiant; gene therapy;
KW   cardiac potassium channel; Jervell and Lange-Nielsen Syndrome; JLN;
KW   chromosome 11p15.5; long QT syndrome.
XX
OS   Homo sapiens.
XX
PN   US6150104-A.
XX
PD   21-NOV-2000.
XX
PF   17-AUG-1998;   98US-0135021.
XX
PR   29-JUL-1998;   98US-0094477.
PR   13-JUN-1997;   97US-0874655.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT, Splawski I;
XX
DR   WPI; 2001-060013/07.
DR   N-PSDB; AAC89984.
XX
PT   DNA encoding for a mutant KVLQT1 which causes Jervell and Lange-Nielsen
PT   syndrome (JLN) when homozygous, useful for diagnosing long QT syndrome,
PT   or diagnosing or prognosing JLN -
XX
PS   Claim 1; Columns 95-100; 58pp; English.
XX
CC   KVLQT1 is a cardiac potassium channel and mutations in the KVLQT1 gene
CC   cause Jervell and Lange-Nielsen Syndrome (JLN). KVLQT1 maps to
CC   chromosome 11p15.5. The present sequence is a mutant KVLQT1. The coding
CC   sequence for the present protein is useful in the diagnosis of long QT
CC   syndrome and in screening humans for the presence of KVLQT1 gene variants
CC   which cause JLN syndrome.
XX
SQ   Sequence   581 AA;

  Query Match             18.4%;  Score 69;  DB 22;  Length 581;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      124 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 183

Qy      245 FVYLAEKDA 253
            |||||||||
Db      184 fvylaekda 192


RESULT   9
AAY57368
ID   AAY57368 standard; Protein; 676 AA.
```

OS Homo sapiens.
XX
PN WO200006600-A1.
XX
PD 10-FEB-2000.
XX
PF 06-OCT-1998; 98WO-US17838.
XX
PR 29-JUL-1998; 98US-0094477.
PR 17-AUG-1998; 98US-0135020.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Keating MT, Sanguinetti MC, Splawski I;
XX
DR WPI; 2000-195262/17.
XX
PT Mutant forms of genes encoding minK protein and KVLQT1 protein involved
PT in cardiac potassium channel formation useful for screening drugs, for
PT preventing and treating cardiac arrhythmia -
XX
PS Disclosure; Fig 10; 167pp; English.
XX
CC The invention relates to KVLQT1 and KCNE1 genes, associated with long
CC QT (LQT) syndrome. It provides a minK protein comprising a mutation which
CC substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
CC Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening
CC KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
CC treating LQT. The ability to predict LQT enables physicians to prevent
CC the diseases with medical therapy such as beta blocking agents and opts
CC for better treatments. The present sequence represents the human
CC KVLQT1 protein fragment.
XX
SQ Sequence 570 AA;

Query Match 18.4%; Score 69; DB 21; Length 570;
Best Local Similarity 100.0%; Pred. No. 6.1e-59;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 113 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 172

Qy 245 FVYLAEKDA 253
|||||||||
Db 173 fvylaekda 181

RESULT 6
AAW33355
ID AAW33355 standard; Protein; 581 AA.
XX
AC AAW33355;
XX
DT 28-FEB-1998 (first entry)
XX
DE Human KVLQT1 associated with long QT syndrome.
XX
KW KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW diagnosis; therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 28..49
FT /label= S1
FT /note= "transmembrane domain"
FT Domain 53..75
FT /label= S2
FT /note= "transmembrane domain"
FT Domain 103..121
FT /label= S3
FT /note= "transmembrane domain"
FT Domain 126..144
FT /label= S4
FT /note= "transmembrane domain"
FT Domain 168..187
FT /label= S5
FT /note= "transmembrane domain"
FT Misc-difference 194
FT /note= "N-glycosylated"
FT Domain 206..225
FT /note= "pore domain"
FT Domain 230..259
FT /label= S6
FT /note= "transmembrane domain"
XX
PN WO9723632-A1.
XX
PD 03-JUL-1997.
XX
PF 20-DEC-1996; 96WO-US19917.
XX
PR 29-OCT-1996; 96US-0739383.
PR 22-DEC-1995; 95US-0019014.
XX
PA (GENZ ) GENZYME GENETICS.
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Connors TD, Curran ME, Keating MF, Landes GM;
XX
DR WPI; 1997-402191/37.
DR N-PSDB; AAT94004.
XX
PT New isolated human potassium channel gene, KVLQT1, - used to develop
PT products for diagnosis, prevention and therapy of long QT syndrome
XX
PS Claim 1; Page 76-78; 105pp; English.
XX
CC This protein comprises a novel human cardiac potassium channel
CC protein. It is encoded by the KVLQT1 gene (see AAT94004) that
CC is associated with long QT syndrome (LQT) gene, an inherited
CC cardiac arrhythmia. KVLQT1 protein coassembles with human minK
CC to form the cardiac IKs potassium channel. IKs dysfunction is
CC a cause of cardiac arrhythmia. Coexpression of KVLQT1 and minK
CC in a host cell provides a means for screening for drugs useful in
CC treating or preventing LQT. The products can also be used for
CC studying mechanisms underlying common arrhythmias and for
CC presymptomatic diagnosis of LQT. Transgenic animals that express
CC human minK and KVQLT1 can be used to test therapeutic agents
CC against LQT.
XX
SQ Sequence 581 AA;

Query Match 18.4%; Score 69; DB 18; Length 581;
Best Local Similarity 100.0%; Pred. No. 6.2e-59;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 183

Qy 245 FVYLAEKDA 253
|||||||||
Db 184 fvylaekda 192

RESULT 7
AAW30038
ID AAW30038 standard; Protein; 581 AA.
XX
AC AAW30038;
XX
DT 12-FEB-1998 (first entry)

```
XX
PF   12-MAY-1999;   99WO-US10260.
XX
PR   29-JUL-1998;   98US-0094477.
PR   17-AUG-1998;   98US-0135010.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
PA   (GENZ ) GENZYME CORP.
XX
PI   Keating MT;  Sanguinetti MC,  Curran ME,  Landes GM,  Connors TD;
PI   Burn TC;  Splawski I;
XX
DR   WPI; 2000-195199/17.
XX
PT   New isolated mutant KVLQT1 nucleic acids, useful for developing
PT   products for the diagnosis, prevention and treatment of long QT
PT   syndrome -
XX
PS   Claim 60; Fig 10; 178pp; English.
XX
CC   The invention relates to KVLQT1 nucleic acids which have a mutation
CC   compared to wild-type KVLQT1 (AAZ98901). The KVLQT1 gene encodes a
CC   protein of 676 amino acids which forms a cardiac I(ks) potassium channel
CC   with the KCNE1 protein (AAY80563). The KCNE1 protein has been shown to
CC   be functional in Xenopus leavis oocyte when KCNE1 DNA is injected into
CC   the egg, indicating that a hommologue of the human KVLQT1 gene is present
CC   in Xenopus. The human KVLQT1 gene was then used to probe a DNA library
CC   to isolate the sequence encoding this protein. Mutations in the KVLQT1
CC   or KCNE1 genes result in cardiac arrhythmias observed as a prolonged QT
CC   curve in electrocardiograms (Long QT syndrome). The genes and proteins
CC   can be used for the diagnosis of subjects with long QT syndrome. They
CC   can also be used to screen for drugs which can be used for treating or
CC   preventing long QT syndrome. The KVLQT1 nucleic acids can be used for
CC   gene therapy, and KVLQT1 peptides can be used for peptide therapy.
XX
SQ   Sequence   376 AA;


  Query Match           100.0%;  Score 376;  DB 21;  Length 376;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  376;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MNENAINSLYEAIPLPQDGSSNGQRQEDRQANSFELKRETLVATDPPRPTINLDPRVSIY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mnenainslyeaiplpqdgssngqrqedrqansfelkretlvatdpprptinldprvsiy 60

Qy      61 SGRRPLFSRTNIQGRVYNFLERPTGWKCFVYHFTVFLIVLICLIFSVLSTIQQYNNLATE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sgrrplfsrtniqgrvynflerptgwkcfvyhftvflivliclifsvlstiqqynnlate 120

Qy     121 TLFWMEIVLVVFFGAEYVVRLWSAGCRSKYVGVWGRLRFARKPISVIDLIVVVASVIVLC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tlfwmeivlvvffgaeyvvrlwsagcrskyvgvwgrlrfarkpisvidlivvvasvivlc 180

Qy     181 VGSNGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 vgsngqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflgli 240

Qy     241 FSSYFVYLAEKDAIDSSGEYQFGSYADALWWGVVTVTTIGYGDKVPQTWIGKTIASCFSV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fssyfvylaekdaidssgeyqfgsyadalwwgvvtvttigygdkvpqtwigktiascfsv 300

Qy     301 FAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSATWKI 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 faisffalpagilgsgfalkvqqkqrqkhfnrqipaaasliqtawrcyaaenpdsatwki 360

Qy     361 YIRKQSRNHHIMSPSP 376
           ||||||||||||||||
Db     361 yirkqsrnhhimspsp 376


RESULT   4
AAY57372
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ID   AAY57372 standard; Protein; 137 AA.
XX
AC   AAY57372;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human KVLQT1 protein fragment.
XX
KW   KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
KW   antiarrhythmic; gene therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO200006600-A1.
XX
PD   10-FEB-2000.
XX
PF   06-OCT-1998;   98WO-US17838.
XX
PR   29-JUL-1998;   98US-0094477.
PR   17-AUG-1998;   98US-0135020.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT;  Sanguinetti MC,  Splawski I;
XX
DR   WPI; 2000-195262/17.
XX
PT   Mutant forms of genes encoding minK protein and KVLQT1 protein involved
PT   in cardiac potassium channel formation useful for screening drugs, for
PT   preventing and treating cardiac arrhythmia -
XX
PS   Disclosure; Fig 3; 167pp; English.
XX
CC   The invention relates to KVLQT1 and KCNE1 genes, associated with long
CC   QT (LQT) syndrome. It provides a minK protein comprising a mutation which
CC   substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
CC   Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening
CC   KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
CC   treating LQT. The ability to predict LQT enables physicians to prevent
CC   the diseases with medical therapy such as beta blocking agents and opts
CC   for better treatments. The present sequence represents the human
CC   KVLQT1 protein fragment.
XX
SQ   Sequence   137 AA;


  Query Match           18.4%;  Score 69;  DB 21;  Length 137;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-59;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 gqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflglifssy 62

Qy     245 FVYLAEKDA 253
           |||||||||
Db      63 fvylaekda 71


RESULT   5
AAY57377
ID   AAY57377 standard; Protein; 570 AA.
XX
AC   AAY57377;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Human KVLQT1 protein fragment.
XX
KW   KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
KW   antiarrhythmic; gene therapy; human.
XX
```

```
PS   Claim 24; Page 72-73; 105pp; English.
XX
CC   This polypeptide comprises the Xenopus homologue of human KVLQT1
CC   (see AAW30038), a protein associated with long QT syndrome (LQT).  A
CC   cDNA clone encoding Xenopus KVLQT1 was isolated from an oocyte cDNA
CC   library by homology to human KVLQT1 cDNA (see AAT90730).  Human
CC   KVLQT1 coassembles with human minK to form a cardiac IKs potassium
CC   channel.  Coexpression of these proteins in a cell can be used to
CC   screen for drugs useful in treating or preventing LQT.
XX
SQ   Sequence   376 AA;


  Query Match             100.0%;  Score 376;  DB 18;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  376;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MNENAINSLYEAIPLPQDGSSNGQRQEDRQANSFELKRETLVATDPPRPTINLDPRVSIY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mnenainslyeaiplpqdgssngqrqedrqansfelkretlvatdpprptinldprvsiy 60

Qy      61 SGRRPLFSRTNIQGRVYNFLERPTGWKCFVYHFTVFLIVLICLIFSVLSTIQQYNNLATE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sgrrplfsrtniqgrvynflerptgwkcfvyhftvflivlicliflsvlstiqqynnlate 120

Qy     121 TLFWMEIVLVVFFGAEYVVRLWSAGCRSKYVGVWGRLRFARKPISVIDLIVVVASVIVLC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tlfwmeivlvvffgaeyvvrlwsagcrskyvgvwgrlrfarkpisvidlivvvasvivlc 180

Qy     181 VGSNGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 vgsngqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflgli 240

Qy     241 FSSYFVYLAEKDAIDSSGEYQFGSYADALWWGVVTVTTIGYGDKVPQTWIGKTIASCFSV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fssyfvylaekdaidssgeyqfgsyadalwwgvvtvttigygdkvpqtwigktiascfsv 300

Qy     301 FAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSATWKI 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 faisffalpagilgsgfalkvqqkqrqkhfnrqipaaasliqtawrcyaaenpdsatwki 360

Qy     361 YIRKQSRNHHIMSPSP 376
           ||||||||||||||||
Db     361 yirkqsrnhhimspsp 376


RESULT   2
AAY57376
ID   AAY57376 standard; Protein; 376 AA.
XX
AC   AAY57376;
XX
DT   19-JUN-2000  (first entry)
XX
DE   Xenopus KVLQT1 partial protein fragment.
XX
KW   KVLQT1; KCNE1; long QT syndrome; LQT syndrome; minK protein;
KW   antiarrhythmic; gene therapy; human; frog.
XX
OS   Xenopus laevis.
XX
PN   WO200006600-A1.
XX
PD   10-FEB-2000.
XX
PF   06-OCT-1998;   98WO-US17838.
XX
PR   29-JUL-1998;   98US-0094477.
PR   17-AUG-1998;   98US-0135020.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Keating MT,  Sanguinetti MC,  Splawski I;
XX
DR   WPI; 2000-195262/17.
XX
PT   Mutant forms of genes encoding minK protein and KVLQT1 protein involved
PT   in cardiac potassium channel formation useful for screening drugs, for
PT   preventing and treating cardiac arrhythmia  -
XX
PS   Disclosure; Fig 10; 167pp; English.
XX
CC   The invention relates to KVLQT1 and KCNE1 genes, associated with long
CC   QT (LQT) syndrome. It provides a minK protein comprising a mutation which
CC   substitutes the wild type amino acids with Leu, Asp, Leu, His, Trp and
CC   Ala or Thr at residues 74,76,28,32,98 and 127 respectively. Screening
CC   KVLQT1 and KCNE1 is useful for identifying mutations for diagnosing and
CC   treating LQT. The ability to predict LQT enables physicians to prevent
CC   the diseases with medical therapy such as beta blocking agents and opts
CC   for better treatments. The present sequence represents a Xenopus
CC   KVLQT1 partial protein fragment.
XX
SQ   Sequence   376 AA;


  Query Match             100.0%;  Score 376;  DB 21;  Length 376;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  376;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MNENAINSLYEAIPLPQDGSSNGQRQEDRQANSFELKRETLVATDPPRPTINLDPRVSIY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mnenainslyeaiplpqdgssngqrqedrqansfelkretlvatdpprptinldprvsiy 60

Qy      61 SGRRPLFSRTNIQGRVYNFLERPTGWKCFVYHFTVFLIVLICLIFSVLSTIQQYNNLATE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 sgrrplfsrtniqgrvynflerptgwkcfvyhftvflivlicliflsvlstiqqynnlate 120

Qy     121 TLFWMEIVLVVFFGAEYVVRLWSAGCRSKYVGVWGRLRFARKPISVIDLIVVVASVIVLC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 tlfwmeivlvvffgaeyvvrlwsagcrskyvgvwgrlrfarkpisvidlivvvasvivlc 180

Qy     181 VGSNGQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLI 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 vgsngqvfatsairgirflqilrmlhvdrqggtwrllgsvvfihrqelittlyigflgli 240

Qy     241 FSSYFVYLAEKDAIDSSGEYQFGSYADALWWGVVTVTTIGYGDKVPQTWIGKTIASCFSV 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 fssyfvylaekdaidssgeyqfgsyadalwwgvvtvttigygdkvpqtwigktiascfsv 300

Qy     301 FAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSATWKI 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 faisffalpagilgsgfalkvqqkqrqkhfnrqipaaasliqtawrcyaaenpdsatwki 360

Qy     361 YIRKQSRNHHIMSPSP 376
           ||||||||||||||||
Db     361 yirkqsrnhhimspsp 376


RESULT   3
AAY80567
ID   AAY80567 standard; Protein; 376 AA.
XX
AC   AAY80567;
XX
DT   06-JUN-2000  (first entry)
XX
DE   partial Xenopus KVLQT1 protein.
XX
KW   KVLQT1; mutation; human; cardiac I(ks) potassium channel; KCNE1; ss;
KW   cardiac arrhythmia; electrocardiogram; Long QT syndrome; gene therapy.
XX
OS   Xenopus laevis.
XX
PN   WO200006199-A1.
XX
PD   10-FEB-2000.
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GenCore version 4.5


OM protein - protein search, using sw model

Run on: November 3, 2001, 10:57:35 ; Search time 33.71 Seconds
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Searched: 412676 seqs, 60623988 residues

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Post-processing: Listing first 45 summaries

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6: /SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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8: /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 376 | 100.0 | 376 | 18 | AAW30036 | Xenopus KVLQT1. X |
| 2 | 376 | 100.0 | 376 | 21 | AAY57376 | Xenopus KVLQT1 par |
| 3 | 376 | 100.0 | 376 | 21 | AAY80567 | partial Xenopus KV |
| 4 | 69 | 18.4 | 137 | 21 | AAY57372 | Human KVLQT1 prote |
| 5 | 69 | 18.4 | 570 | 21 | AAY57377 | Human KVLQT1 prote |
| 6 | 69 | 18.4 | 581 | 18 | AAW33355 | Human KVLQT1 assoc |
| 7 | 69 | 18.4 | 581 | 18 | AAW30038 | Human KVLQT1 assoc |
| 8 | 69 | 18.4 | 581 | 22 | AAB49499 | Mutant human KVLQT |
| 9 | 69 | 18.4 | 676 | 21 | AAY57368 | Human KVLQT1 prote |
| 10 | 69 | 18.4 | 676 | 21 | AAY80562 | Human long QT synd |
| 11 | 69 | 18.4 | 676 | 22 | AAB49494 | Human KVLQT1. Hom |
| 12 | 69 | 18.4 | 677 | 20 | AAY08343 | Human KCNQ1 protei |
| 13 | 21 | 5.6 | 21 | 21 | AAB11385 | Potassium channel |
| 14 | 21 | 5.6 | 283 | 22 | AAB49495 | Mutant human KVLQT |
| 15 | 21 | 5.6 | 807 | 20 | AAY08342 | Human nKTQ1 protei |
| 16 | 20 | 5.3 | 695 | 21 | AAB01476 | KCNQ4 Potassium ch |
| 17 | 20 | 5.3 | 846 | 21 | AAB24241 | Human KCNQ5 (KCN6q |
| 18 | 20 | 5.3 | 897 | 22 | AAB47046 | Human KCNQ5 potass |
| 19 | 19 | 5.1 | 245 | 20 | AAY01531 | Amino acid sequenc |
| 20 | 19 | 5.1 | 393 | 18 | AAW14282 | Human K+ channel p |
| 21 | 19 | 5.1 | 722 | 20 | AAY01530 | Amino acid sequenc |
| 22 | 19 | 5.1 | 757 | 20 | AAY08345 | Mouse partial KCNQ |
| 23 | 19 | 5.1 | 854 | 20 | AAY23215 | Human brain-derive |
| 24 | 19 | 5.1 | 871 | 20 | AAY01529 | Amino acid sequenc |
| 25 | 19 | 5.1 | 872 | 20 | AAY08341 | Human KCNQ2 protei |
| 26 | 19 | 5.1 | 930 | 20 | AAY08347 | Human mutant KCNQ2 |
| 27 | 17 | 4.5 | 61 | 21 | AAY57371 | Human KVLQT1 prote |
| 28 | 15 | 4.0 | 15 | 20 | AAY34136 | Variant human pota |
| 29 | 13 | 3.5 | 854 | 20 | AAY01534 | Amino acid sequenc |
| 30 | 13 | 3.5 | 870 | 20 | AAY08346 | Mouse KCNQ3 protei |
| 31 | 13 | 3.5 | 872 | 20 | AAY08344 | Human KCNQ3 protei |
| 32 | 10 | 2.7 | 26 | 21 | AAY57370 | Human KVLQT1 prote |
| 33 | 8 | 2.1 | 1600 | 21 | AAG51095 | Arabidopsis thalia |
| 34 | 8 | 2.1 | 1608 | 21 | AAG51094 | Arabidopsis thalia |
| 35 | 8 | 2.1 | 1625 | 21 | AAG51093 | Arabidopsis thalia |
| 36 | 7 | 1.9 | 14 | 15 | AAR52597 | Hepatitis E virus |
| 37 | 7 | 1.9 | 67 | 20 | AAY11640 | Human 5' EST secre |
| 38 | 7 | 1.9 | 74 | 20 | AAY35977 | Extended human sec |
| 39 | 7 | 1.9 | 98 | 21 | AAB16753 | Bacteriophage Dp-1 |
| 40 | 7 | 1.9 | 119 | 19 | AAW69227 | NADH dehydrogenase |
| 41 | 7 | 1.9 | 143 | 21 | AAY54054 | Angiostatin-bindin |
| 42 | 7 | 1.9 | 261 | 20 | AAY06553 | Phage lambda red b |
| 43 | 7 | 1.9 | 275 | 15 | AAR60476 | Serine protease of |
| 44 | 7 | 1.9 | 327 | 17 | AAR96093 | Hepatitis E virus |
| 45 | 7 | 1.9 | 327 | 18 | AAW35820 | Hepatitis E virus |

ALIGNMENTS

RESULT 1
AAW30036
ID AAW30036 standard; protein; 376 AA.
XX
AC AAW30036;
XX
DT 12-FEB-1998 (first entry)
XX
DE Xenopus KVLQT1.
XX
KW KVLQT1; long QT syndrome; arrhythmia; minK; potassium channel;
KW diagnosis; therapy.
XX
OS Xenopus sp.
XX
PN WO9723598-A2.
XX
PD 03-JUL-1997.
XX
PF 20-DEC-1996; 96WO-US19756.
XX
PR 29-OCT-1996; 96US-0739383.
PR 22-DEC-1995; 95US-0019014.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Curran ME, Keating MT, Sanguinetti MC;
XX
DR WPI; 1997-402190/37.
XX
PT Human minK and Xenopus KVLQT1 coding sequences - used for assays for
PT identifying drugs which can be used for preventing or treating long
PT QT syndrome
XX

```
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     196 IRFLQIL 202
           |||||||
Db      13 IRFLQIL 19


RESULT  15
TBPA_HAEIN
ID   TBPA_HAEIN     STANDARD;      PRT;   332 AA.
AC   P44984;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   THIAMINE-BINDING PERIPLASMIC PROTEIN PRECURSOR.
GN   TBPA OR HI1019.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC   Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RD / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus
RT   influenzae Rd.";
RL   Science 269:496-512(1995).
CC   -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC       TBPA-THIPQ FOR THIAMINE AND TPP (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: PERIPLASMIC.
CC   -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC       PROTEIN FAMILY 1.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U32782; AAC22678.1; -.
DR   TIGR; HI1019; -.
DR   InterPro; IPR000567; -.
DR   PROSITE; PS01037; SBP_BACTERIAL_1; 1.
KW   Transport; Periplasmic; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    332       THIAMINE-BINDING PERIPLASMIC PROTEIN.
SQ   SEQUENCE   332 AA;  37272 MW;  90A27B35D0F9C741 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 332;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     318 ALKVQQK 324
           |||||||
Db     299 ALKVQQK 305


Search completed: November  2, 2001, 12:12:02
Job time: 598 sec
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CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; J02058; -; NOT_ANNOTATED_CDS.
DR   PIR; A04168; QQOMC2.
DR   InterPro; IPR000263; -.
DR   InterPro; IPR001530; -.
DR   InterPro; IPR003001; -.
DR   Pfam; PF01489; Gemini_BR1; 1.
DR   PRINTS; PR00223; GEMCOATARBR1.
DR   PRINTS; PR00225; GEMCOATBR1.
SQ   SEQUENCE   256 AA;  29305 MW;  070A364569507634 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    362 IRKQSRN 368
          |||||||
Db      4 IRKQSRN 10


RESULT  13
VBET_LAMBD
ID   VBET_LAMBD     STANDARD;      PRT;   261 AA.
AC   P03698;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RECOMBINATION PROTEIN BET.
GN   BET OR BETA OR RED-BETA OR REDB.
OS   Bacteriophage lambda.
OC   Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
OC   Lambda phage group.
OX   NCBI_TaxID=10710;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83189071; PubMed=6221115;
RA   Sanger F., Coulson A.R., Hong G.F., Hill D.F., Petersen G.B.;
RT   "Nucleotide sequence of bacteriophage lambda DNA.";
RL   J. Mol. Biol. 162:729-773(1982).
RN   [2]
RP   SEQUENCE OF 1-103 FROM N.A.
RX   MEDLINE=82059489; PubMed=6458018;
RA   Ineichen K., Shepherd J.C.W., Bickle T.A.;
RT   "The DNA sequence of the phage lambda genome between PL and the gene
RT   bet.";
RL   Nucleic Acids Res. 9:4639-4653(1981).
CC   -!- FUNCTION: GENE BET PROTEIN FUNCTIONS IN GENERAL RECOMBINATION AND
CC       IN THE LATE, ROLLING-CIRCLE MODE OF LAMBDA DNA REPLICATION.
CC       HAS A FUNCTION SIMILAR TO THAT OF E.COLI RECT. IT IS A SINGLE-
CC       STRANDED DNA BINDING PROTEIN THAT CAN PROMOTE RENATURATION OF DNA.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; J02459; AAA96570.1; -.
DR   EMBL; V00638; CAA23976.1; -.
DR   PIR; A04320; QBBPL.
KW   DNA recombination; DNA-binding.
SQ   SEQUENCE   261 AA;  29688 MW;  99583014F97330A6 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    226 QELITTL 232
          |||||||
Db     24 QELITTL 30


RESULT  14
PLSC_MYCGE
ID   PLSC_MYCGE     STANDARD;      PRT;   268 AA.
AC   Q49402; Q49287;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   PROBABLE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
DE   (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID
DE   ACYLTRANSFERASE) (LPAAT).
GN   PLSC OR MG212.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC   Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
RN   [2]
RP   SEQUENCE OF 1-105 FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=94075230; PubMed=8253680;
RA   Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT   "A survey of the Mycoplasma genitalium genome by using random
RT   sequencing.";
RL   J. Bacteriol. 175:7918-7930(1993).
CC   -!- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATIDIC
CC       ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION.
CC   -!- CATALYTIC ACTIVITY: ACYL-COA + 1-ACYL-SN-GLYCEROL 3-PHOSPHATE =
CC       COA + 1,2-DIACYL-SN-GLYCEROL 3-PHOSPHATE.
CC   -!- PATHWAY: SECOND STEP IN DE NOVO PHOSPHOLIPID BIOSYNTHESIS.
CC   -!- SIMILARITY: BELONGS TO THE 1-ACYL-SN-GLYCEROL-3-PHOSPHATE
CC       ACYLTRANSFERASE FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U39701; AAC71431.1; -.
DR   EMBL; U02160; AAD12442.1; -.
DR   TIGR; MG212; -.
DR   InterPro; IPR002123; -.
DR   Pfam; PF01553; Acyltransferase; 1.
KW   Phospholipid biosynthesis; Transferase; Acyltransferase.
FT   CONFLICT      2      2       MISSING (IN REF. 2).
SQ   SEQUENCE   268 AA;  30469 MW;  A88B07D2BC4C6A4A CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 268;
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FT   DOMAIN      122    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    160       POTENTIAL.
FT   DOMAIN      161    177       LUMENAL (POTENTIAL).
FT   BINDING     147    147       DICYCLOHEXYLCARBODIIMIDE (POTENTIAL).
SQ   SEQUENCE   177 AA;  18131 MW;  32521191B721FB52 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 177;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     100 LICLIFS 106
           |||||||
Db     140 LICLIFS 146


RESULT  10
YZ12_METJA
ID   YZ12_METJA     STANDARD;      PRT;   241 AA.
AC   Q60274;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   HYPOTHETICAL PROTEIN MJECL12.
GN   MJECL12.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC   Methanococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L77118; AAC37085.1; -.
DR   TIGR; MJECL12; -.
KW   Hypothetical protein.
SQ   SEQUENCE   241 AA;  27268 MW;  C5D3C7742A35A097 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      33 SFELKRE 39
           |||||||
Db     148 SFELKRE 154


RESULT  11
ATP6_BACSU
ID   ATP6_BACSU     STANDARD;      PRT;   244 AA.
AC   P37813;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).
GN   ATPB.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group;
OC   Bacillus/Staphylococcus group; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=168;
RX   MEDLINE=95050246; PubMed=7961438;
RA   Santana M., Ionescu M.S., Vertes A., Longin R., Kunst F., Danchin A.,
RA   Glaser P.;
RT   "Bacillus subtilis F0F1 ATPase: DNA sequence of the atp operon and
RT   characterization of atp mutants.";
RL   J. Bacteriol. 176:6802-6811(1994).
CC   -!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC       DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC   -!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC       CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC       SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC       HAS THREE MAIN SUBUNITS: A, B AND C.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 8
CC       POTENTIAL TRANSMEMBRANE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z28592; CAA82254.1; -.
DR   EMBL; Z99122; CAB15704.1; -.
DR   PIR; S39250; S39250.
DR   SubtiList; BG10815; atpB.
DR   InterPro; IPR000568; -.
DR   Pfam; PF00119; ATP-synt_A; 1.
DR   PROSITE; PS00449; ATPASE_A; 1.
KW   Hydrogen ion transport; CF(0); Transmembrane.
SQ   SEQUENCE   244 AA;  27054 MW;  E26172BA9F1AA248 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 244;
  Best Local Similarity   100.0%;  Pred. No. 21;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     173 VASVIVL 179
           |||||||
Db      25 VASVIVL 31


RESULT  12
VBR1_CLVK
ID   VBR1_CLVK      STANDARD;      PRT;   256 AA.
AC   P03565;
DT   [illegible]-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   BR1 PROTEIN (29.4 KDA PROTEIN).
GN   BV1.
OS   Cassava latent virus (strain West Kenyan 844).
OC   Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX   NCBI_TaxID=10818;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Stanley J., Gay M.R.;
RT   "Nucleotide sequence of cassava latent virus DNA.";
RL   Nature 301:260-262(1983).
CC   -!- SIMILARITY: BELONGS TO GEMINIVIRUSES BR1 PROTEIN FAMILY.
```

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DR   PROSITE; PS00598; CHROMO_1; 1.
DR   PROSITE; PS50013; CHROMO_2; 2.
KW   Chromatin regulator; Nuclear protein; Transcription regulation;
KW   Repressor; Phosphorylation.
FT   DOMAIN       20     78       CHROMO.
FT   DOMAIN      111    169       CHROMO SHADOW DOMAIN.
SQ   SEQUENCE   173 AA;  19720 MW;  EB9D2F554F58C897 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 173;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     253 AIDSSGE 259
           |||||||
Db     119 AIDSSGE 125


RESULT   8
VATL_ENTDI
ID   VATL_ENTDI     STANDARD;      PRT;   176 AA.
AC   Q24808;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   VACUOLAR ATP SYNTHASE 16 KDA PROTEOLIPID SUBUNIT (EC 3.6.1.34) (V-
DE   ATPASE 16 KDA PROTEOLIPID SUBUNIT).
GN   VMA3.
OS   Entamoeba dispar.
OC   Eukaryota; Entamoebidae; Entamoeba.
OX   NCBI_TaxID=46681;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NON-PATHOGENIC;
RX   MEDLINE=94314485; PubMed=8039932;
RA   Descoteaux S., Yu Y., Samuelson J.;
RT   "Cloning of Entamoeba genes encoding proteolipids of putative
RT   vacuolar proton-translocating ATPases.";
RL   Infect. Immun. 62:3572-3575(1994).
CC   -!- FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE
CC       INTEGRAL V0 COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE
CC       FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN
CC       EUKARYOTIC CELLS.
CC   -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
CC       PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
CC       C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
CC       COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS PRESENT
CC       AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR.
CC   -!- MISCELLANEOUS: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIIMIDE (DCDD)
CC       WHICH INHIBITS THE ATPASE (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U01055; AAA21448.1; -.
DR   InterPro; IPR000245; -.
DR   InterPro; IPR002379; -.
DR   Pfam; PF00137; ATP-synt_C; 2.
DR   PRINTS; PR00122; VACATPASE.
KW   Hydrolase; Hydrogen ion transport; ATP synthesis; Transmembrane.
FT   DOMAIN       1     17       LUMENAL (POTENTIAL).
FT   TRANSMEM    18     38       POTENTIAL.
FT   DOMAIN      39     62       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    63     83       POTENTIAL.
FT   DOMAIN      84     98       LUMENAL (POTENTIAL).
FT   TRANSMEM    99    119       POTENTIAL.
FT   DOMAIN     120    136       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   137    157       POTENTIAL.
FT   DOMAIN     158    176       LUMENAL (POTENTIAL).
FT   BINDING    145    145       DICYCLOHEXYLCARBODIIMIDE (POTENTIAL).
FT   SITE       145    145       ESSENTIAL FOR ENZYME AND TRANSPORT
FT                               ACTIVITY (BY SIMILARITY).
SQ   SEQUENCE   176 AA;  18103 MW;  50132CC98FD0E850 CRC64;


  Query Match             1.9%;  Score 7;  DB 1;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 16;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     100 LICLIFS 106
           |||||||
Db     138 LICLIFS 144


RESULT   9
VATL_ENTHI
ID   VATL_ENTHI     STANDARD;      PRT;   177 AA.
AC   Q24810;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   VACUOLAR ATP SYNTHASE 16 KDA PROTEOLIPID SUBUNIT (EC 3.6.1.34) (V-
DE   ATPASE 16 KDA PROTEOLIPID SUBUNIT).
GN   VMA3.
OS   Entamoeba histolytica.
OC   Eukaryota; Entamoebidae; Entamoeba.
OX   NCBI_TaxID=5759;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HM-1:IMSS;
RX   MEDLINE=94314485; PubMed=8039932;
RA   Descoteaux S., Yu Y., Samuelson J.;
RT   "Cloning of Entamoeba genes encoding proteolipids of putative
RT   vacuolar proton-translocating ATPases.";
RL   Infect. Immun. 62:3572-3575(1994).
CC   -!- FUNCTION: PROTON-CONDUCTING PORE FORMING SUBUNIT OF THE MEMBRANE
CC       INTEGRAL V0 COMPLEX OF VACUOLAR ATPASE. V-ATPASE IS RESPONSIBLE
CC       FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN
CC       EUKARYOTIC CELLS.
CC   -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
CC       PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
CC       C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
CC       COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN; WHICH IS PRESENT
CC       AS A HEXAMER THAT FORMS THE PROTON-CONDUCTING PORE).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. VACUOLAR.
CC   -!- MISCELLANEOUS: THIS SUBUNIT BINDS DICYCLOHEXYLCARBODIIMIDE (DCDD)
CC       WHICH INHIBITS THE ATPASE (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE V-ATPASE PROTEOLIPID SUBUNIT FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U01057; AAA21450.1; -.
DR   InterPro; IPR000245; -.
DR   InterPro; IPR002379; -.
DR   Pfam; PF00137; ATP-synt_C; 2.
DR   PRINTS; PR00122; VACATPASE.
KW   Hydrolase; Hydrogen ion transport; ATP synthesis; Transmembrane.
FT   DOMAIN       1     19       LUMENAL (POTENTIAL).
FT   TRANSMEM    20     40       POTENTIAL.
FT   DOMAIN      41     64       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    65     85       POTENTIAL.
FT   DOMAIN      86    100       LUMENAL (POTENTIAL).
FT   TRANSMEM   101    121       POTENTIAL.
```

```
RA   Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA   Daniels D.L.;
RT   "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT   region from 89.2 to 92.8 minutes.";
RL   Nucleic Acids Res. 21:5408-5417(1993).
CC   -!- SIMILARITY: BELONGS TO THE YBGE/YHDA/YHJK/YJCC FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U00006; AAC43155.1; -.
DR   EMBL; AE000479; AAC77031.1; -.
DR   EcoGene; EG11938; yjcC.
DR   InterPro; IPR001633; -.
DR   Pfam; PF00563; DUF2; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   528 AA;  60801 MW;  F6E4819954912F31 CRC64;


  Query Match              2.7%;  Score 10;  DB 1;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     306 FALPAGILGS 315
           ||||||||||
Db     245 FALPAGILGS 254


RESULT   6
N4BM_HUMAN
ID   N4BM_HUMAN     STANDARD;      PRT;   119 AA.
AC   O95298;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3)
DE   (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).
GN   NDUFC2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99097250; PubMed=9878551;
RA   Loeffen J.L.C.M., Triepels R.H., van den Heuvel L., Schuelke M.,
RA   Buskens C.A.F., Smeets R.J.P., Trijbels J.M.F., Smeitink J.A.M.;
RT   "cDNA of eight nuclear encoded subunits of NADH:Ubiquinone
RT   oxidoreductase: human complex I cDNA characterization completed.";
RL   Biochem. Biophys. Res. Commun. 253:415-422(1998).
CC   -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC       CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS
CC       BELIEVED TO BE UBIQUINONE.
CC   -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC   -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 41 DIFFERENT SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE; MATRIX SIDE.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF087659; AAD09754.1; -.
DR   MIM; 603845; -.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ   SEQUENCE   119 AA;  14187 MW;  9A47DEE33DC9244D CRC64;


  Query Match              1.9%;  Score 7;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     232 LYIGFLG 238
           |||||||
Db      31 LYIGFLG 37


RESULT   7
CBX3_HUMAN
ID   CBX3_HUMAN     STANDARD;      PRT;   173 AA.
AC   Q13185; Q99409;
DT   01-NOV-1997 (Rel. 35, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   CHROMOBOX PROTEIN HOMOLOG 3 (HETEROCHROMATIN PROTEIN 1 HOMOLOG GAMMA)
DE   (HP1 GAMMA) (MODIFIER 2 PROTEIN).
GN   CBX3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96278941; PubMed=8663349;
RA   Ye Q., Worman H.J.;
RT   "Interaction between an integral protein of the nuclear envelope
RT   inner membrane and human chromodomain proteins homologous to
RT   Drosophila HP1.";
RL   J. Biol. Chem. 271:14653-14656(1996).
RN   [2]
RP   REVISIONS.
RA   Ye Q., Worman H.J.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20130009; PubMed=10664448;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of HP1.";
RL   FEBS Lett. 467:17-21(2000).
CC   -!- FUNCTION: COMPONENT OF HETEROCHROMATIN. MAY INTERACT WITH LAMIN B
CC       RECEPTOR (LBR). THIS INTERACTION CAN CONTRIBUTE TO THE ASSOCIATION
CC       OF THE HETEROCHROMATIN WITH THE INNER NUCLEAR MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC   -!- PTM: PHOSPHORYLATION OF HP1 AND LBR MAY BE RESPONSIBLE FOR SOME OF
CC       THE ALTERATIONS IN CHROMATIN ORGANIZATION AND NUCLEAR STRUCTURE
CC       WHICH OCCUR AT VARIOUS TIMES DURING THE CELL CYCLE. PHOSPHORYLATED
CC       BY PIM-1.
CC   -!- SIMILARITY: CONTAINS 1 'CHROMO' DOMAIN AND 1 'CHROMO SHADOW'
CC       DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U26312; AAB48101.1; -.
DR   EMBL; AB030905; BAA83340.1; -.
DR   MIM; 604477; -.
DR   HSSP; P23197; 1AP0.
DR   InterPro; IPR000953; -.
DR   Pfam; PF01393; Chromo_shadow; 1.
DR   Pfam; PF00385; chromo; 1.
DR   PRINTS; PR00504; CHROMODOMAIN.
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DR   EMBL; AF105212; AAD14681.1; JOINED.
DR   EMBL; AF105213; AAD14681.1; JOINED.
DR   EMBL; AF105214; AAD14681.1; JOINED.
DR   EMBL; AF105215; AAD14681.1; JOINED.
DR   MIM; 603537; -.
DR   MIM; 600101; -.
DR   InterPro; IPR000636; -.
DR   InterPro; IPR003091; -.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Multigene family; Disease mutation; Deafness.
FT   TRANSMEM     45     65       POTENTIAL.
FT   TRANSMEM     98    118       POTENTIAL.
FT   TRANSMEM    132    152       POTENTIAL.
FT   TRANSMEM    173    193       POTENTIAL.
FT   TRANSMEM    238    258       POTENTIAL.
FT   TRANSMEM    298    318       POTENTIAL.
FT   VARIANT     276    276       W -> S (IN DFNA2).
FT                                /FTId=VAR_008726.
FT   VARIANT     285    285       G -> C (IN DFNA2; LOSS OF POTASSIUM
FT                                SELECTIVITY OF THE PORE).
FT                                /FTId=VAR_008727.
FT   VARIANT     285    285       G -> S (IN DFNA2).
FT                                /FTId=VAR_001547.
FT   VARIANT     321    321       G -> S (IN DFNA2).
FT                                /FTId=VAR_008728.
SQ   SEQUENCE   695 AA;  77091 MW;  A58737BD845E1A3A CRC64;


  Query Match             5.3%;  Score 20;  DB 1;  Length 695;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     303 ISFFALPAGILGSGFALKVQ 322
           ||||||||||||||||||||
Db     308 ISFFALPAGILGSGFALKVQ 327


RESULT   4
CIQ3_HUMAN
ID   CIQ3_HUMAN     STANDARD;      PRT;   872 AA.
AC   O43525;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 3.
GN   KCNQ3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99087323; PubMed=9872318;
RA   Schroeder B.C., Kubisch C., Stein V., Jentsch T.J.;
RT   "Moderate loss of function of cyclic-AMP-modulated KCNQ2/KCNQ3 K+
RT   channels causes epilepsy.";
RL   Nature 396:687-690(1998).
RN   [2]
RP   SEQUENCE OF 48-872 FROM N.A., AND VARIANT EBN2 VAL-310.
RX   MEDLINE=98085869; PubMed=9425900;
RA   Charlier C., Singh N.A., Ryan S.G., Lewis T.B., Reus B.E., Leach R.J.,
RA   Leppert M.;
RT   "A pore mutation in a novel KQT-like potassium channel gene in an
RT   idiopathic epilepsy family.";
RL   Nat. Genet. 18:53-55(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC       CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC       EVERY THIRD POSITION (BY SIMILARITY).
CC   -!- DISEASE: DEFECTS IN KCNQ3 ARE THE CAUSE OF BENIGN FAMILIAL
CC       NEONATAL CONVULSIONS TYPE 2 (BFNC2); ALSO KNOWN AS EPILEPSY,
CC       BENIGN NEONATAL TYPE 2 (EBN2) BFNC2 IS AN AUTOSOMAL-DOMINANT
CC       DISEASE.
CC   -!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC       CLASS. KQT SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF071491; AAC96101.1; -.
DR   EMBL; AF071478; AAC96101.1; JOINED.
DR   EMBL; AF071479; AAC96101.1; JOINED.
DR   EMBL; AF071480; AAC96101.1; JOINED.
DR   EMBL; AF071481; AAC96101.1; JOINED.
DR   EMBL; AF071482; AAC96101.1; JOINED.
DR   EMBL; AF071483; AAC96101.1; JOINED.
DR   EMBL; AF071484; AAC96101.1; JOINED.
DR   EMBL; AF071485; AAC96101.1; JOINED.
DR   EMBL; AF071486; AAC96101.1; JOINED.
DR   EMBL; AF071487; AAC96101.1; JOINED.
DR   EMBL; AF071488; AAC96101.1; JOINED.
DR   EMBL; AF071489; AAC96101.1; JOINED.
DR   EMBL; AF071490; AAC96101.1; JOINED.
DR   EMBL; AF033347; AAB97314.1; -.
DR   MIM; 602232; -.
DR   MIM; 121201; -.
DR   InterPro; IPR000636; -.
DR   InterPro; IPR003091; -.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR00169; KCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW   Multigene family; Disease mutation.
FT   TRANSMEM    122    142       POTENTIAL.
FT   TRANSMEM    153    173       POTENTIAL.
FT   TRANSMEM    197    217       POTENTIAL.
FT   TRANSMEM    262    282       POTENTIAL.
FT   TRANSMEM    300    320       POTENTIAL.
FT   TRANSMEM    331    351       POTENTIAL.
FT   VARIANT     310    310       G -> V (IN BFNC2).
FT                                /FTId=VAR_001546.
SQ   SEQUENCE   872 AA;  96742 MW;  BB79C69EE8591A84 CRC64;


  Query Match             3.5%;  Score 13;  DB 1;  Length 872;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     304 SFFALPAGILGSG 316
           |||||||||||||
Db     342 SFFALPAGILGSG 354


RESULT   5
YJCC_ECOLI
ID   YJCC_ECOLI     STANDARD;      PRT;   528 AA.
AC   P32701; P76789;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   HYPOTHETICAL 60.8 KDA PROTEIN IN SSB-SOXS INTERGENIC REGION (O528).
GN   YJCC.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=94089392; PubMed=8265357;
```

```
RT   "Molecular genetics of the long QT syndrome: two novel mutations of
RT   the KVLQT1 gene and phenotypic expression of the mutant gene in a
RT   large kindred.";
RL   Hum. Mutat. 11:158-165(1998).
RN   [16]
RP   VARIANT LQT1 PHE-339 DEL.
RX   MEDLINE=98366466; PubMed=9702906;
RA   Ackerman M.J., Schroeder J.J., Berry R., Schaid D.J., Porter C.-B.J.,
RA   Michels V.V., Thibodeau S.N.;
RT   "A novel mutation in KVLQT1 is the molecular basis of inherited long
RT   QT syndrome in a near-drowning patient's family.";
RL   Pediatr. Res. 44:148-153(1998).
RN   [17]
RP   VARIANT LQT1 THR-525.
RX   MEDLINE=99415293; PubMed=10482963;
RA   Larsen L.A., Fosdal I., Andersen P.S., Kanters J.K., Vuust J.,
RA   Wettrell G., Christiansen M.;
RT   "Recessive Romano-Ward syndrome associated with compound
RT   heterozygosity for two mutations in the KVLQT1 gene.";
RL   Eur. J. Hum. Genet. 7:724-728(1999).
RN   [18]
RP   VARIANTS LQT1 S-184; R-189; S-314; S-315; R-345; P-373 AND R-392.
RX   MEDLINE=99235550; PubMed=10220144;
RA   Jongbloed R.J.E., Wilde A.A.M., Geelen J.L.M.C., Doevendans P.,
RA   Schaap C., van Langen I., van Tintelen J.P., Cobben J.M.,
RA   Beaufort-Krol G.C.M., Geraedts J.P.M., Smeets H.J.M.;
RT   "Novel KCNQ1 and HERG missense mutations in Dutch long-QT families.";
RL   Hum. Mutat. 13:301-310(1999).
RN   [19]
RP   VARIANT LQT1 CYS-157.
RX   MEDLINE=99235552; PubMed=10220146;
RA   Larsen L.A., Christiansen M., Vuust J., Andersen P.S.;
RT   "High-throughput single-strand conformation polymorphism analysis by
RT   automated capillary electrophoresis: robust multiplex analysis and
RT   pattern-based identification of allelic variants.";
RL   Hum. Mutat. 13:318-327(1999).
RN   [20]
RP   VARIANTS LQT1 GLN-190; HIS-243; TRP-533 AND TRP-539.
RX   MEDLINE=20192667; PubMed=10728423;
RA   Chouabe C., Neyroud N., Richard P., Denjoy I., Hainque B., Romey G.,
RA   Drici M.D., Guicheney P., Barhanin J.;
RT   "Novel mutations in KvLQT1 that affect Iks activation through
RT   interactions with Isk.";
RL   Cardiovasc. Res. 45:971-980(2000).
RN   [21]
RP   VARIANTS LQT1.
RX   MEDLINE=20432616; PubMed=10973849;
RA   Splawski I., Shen J., Timothy K.W., Lehmann M.H., Priori S.,
RA   Robinson J.L., Moss A.J., Schwartz P.J., Towbin J.A., Vincent G.M.,
RA   Keating M.T.;
RT   "Spectrum of mutations in long-QT syndrome genes. KVLQT1, HERG, SCN5A,
RT   KCNE1, and KCNE2.";
RL   Circulation 102:1178-1185(2000).
CC   -!- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
CC       WITH KCNE1 (MINK) TO FORM THE I(KS) CARDIAC POTASSIUM CURRENT.
CC       ELICITS A RAPIDLY ACTIVATING, K(+)-SELECTIVE OUTWARD CURRENT.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY
CC       ALTERNATIVE SPLICING. TKVLQT1 IS A TRUNCATED ISOFORM THAT IS
CC       NONFUNCTIONAL ALONE BUT MODULATORY WHEN COEXPRESSED WITH THE FULL-
CC       LENGTH ISOFORM.
CC   -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC       CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC       EVERY THIRD POSITION.
CC   -!- DISEASE: DEFECTS IN KCNQ1 IS THE CAUSE OF LONG QT SYNDROME TYPE 1
CC       (LQT1 OR LQTS). LQT1 IS A CONGENITAL HEART DISEASE WITH FREQUENT
CC       FAMILIAL TRANSMISSION AND IS CHARACTERIZED BY A PROLONGED QT
CC       INTERVAL IN THE ELECTROCARDIOGRAM WHICH CAUSES ABNORMAL

  Query Match           18.4%;  Score 69;  DB 1;  Length 676;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-62;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      185 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 244
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      219 GQVFATSAIRGIRFLQILRMLHVDRQGGTWRLLGSVVFIHRQELITTLYIGFLGLIFSSY 278

Qy      245 FVYLAEKDA 253
            |||||||||
Db      279 FVYLAEKDA 287


RESULT   3
CIQ4_HUMAN
ID   CIQ4_HUMAN     STANDARD;      PRT;   695 AA.
AC   P56696; O96025;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 4.
GN   KCNQ4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT DFNA2 SER-285.
RX   MEDLINE=99148276; PubMed=10025409;
RA   Kubisch C., Schroeder B.C., Friedrich T., Luetjohann B.,
RA   El-Amraoui A., Marlin S., Petit C., Jentsch T.J.;
RT   "KCNQ4, a novel potassium channel expressed in sensory outer hair
RT   cells, is mutated in dominant deafness.";
RL   Cell 96:437-446(1999).
RN   [2]
RP   VARIANTS DFNA2 SER-276; CYS-285 AND SER-321.
RX   MEDLINE=99299248; PubMed=10369879;
RA   Coucke P.J., Van Hauwe P., Kelley P.M., Kunst H., Schatteman I.,
RA   Van Velzen D., Meyers J., Ensink R.J., Verstreken M., Declau F.,
RA   Marres H., Kastury K., Bhasin S., McGuirt W.T., Smith R.J.H.,
RA   Cremers C.W.R.J., Van de Heyning P., Willems P.J., Smith S.D.,
RA   Van Camp G.;
RT   "Mutations in the KCNQ4 gene are responsible for autosomal dominant
RT   deafness in four DFNA2 families.";
RL   Hum. Mol. Genet. 8:1321-1328(1999).
CC   -!- FUNCTION: MAY BE RESPONSIBLE FOR POTASSIUM IONS AFTER STIMULATION
CC       OF THE HAIR CELL.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN THE OUTER, BUT NOT THE INNER,
CC       SENSORY HAIR CELLS OF THE COCHLEA.
CC   -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC       CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC       EVERY THIRD POSITION (BY SIMILARITY).
CC   -!- DISEASE: DEFECTS IN KCNQ4 ARE A CAUSE OF AUTOSOMAL DOMINANT
CC       NONSYNDROMIC SENSORINEURAL DEAFNESS TYPE 2 (DFNA2).
CC   -!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC       CLASS. KQT SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF105202; AAD14680.1; -.
DR   EMBL; AF105216; AAD14681.1; -.
DR   EMBL; AF105203; AAD14681.1; JOINED.
DR   EMBL; AF105204; AAD14681.1; JOINED.
DR   EMBL; AF105205; AAD14681.1; JOINED.
DR   EMBL; AF105206; AAD14681.1; JOINED.
DR   EMBL; AF105207; AAD14681.1; JOINED.
DR   EMBL; AF105208; AAD14681.1; JOINED.
DR   EMBL; AF105209; AAD14681.1; JOINED.
DR   EMBL; AF105210; AAD14681.1; JOINED.
DR   EMBL; AF105211; AAD14681.1; JOINED.
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  Best Local Similarity   100.0%;  Pred. No. 1.3e-64;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     291 GKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAA 350
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     260 GKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAA 319

Qy     351 ENPDSATWKIY 361
           ||||||||||||
Db     320 ENPDSATWKIY 330


RESULT   2
CIQ1_HUMAN
ID   CIQ1_HUMAN     STANDARD;      PRT;   676 AA.
AC   P51787; Q92960; O00347; O60607;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   01-OCT-2000 (Rel. 40, Last annotation update)
DE   VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 1 (KV1.9).
GN   KCNQ1 OR KCNA9 OR KVLQT1 OR KCNA8.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97459933; PubMed=9312006;
RA   Chouabe C., Neyroud N., Guicheney P., Lazdunski M., Romey G.,
RA   Barhanin J.;
RT   "Properties of KvLQT1 K+ channel mutations in Romano-Ward and Jervell
RT   and Lange-Nielsen inherited cardiac arrhythmias.";
RL   EMBO J. 16:5472-5479(1997).
RN   [2]
RP   SEQUENCE OF 96-156 FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=97055938; PubMed=8900283;
RA   Sanguinetti M.C., Curran M.E., Zou A., Shen J., Spector P.S.,
RA   Atkinson D.L., Keating M.T.;
RT   "Coassembly of K(V)LQT1 and minK (IsK) proteins to form cardiac I(Ks)
RT   potassium channel.";
RL   Nature 384:80-83(1996).
RN   [3]
RP   SEQUENCE OF 1-129 FROM N.A.
RX   MEDLINE=97268689; PubMed=9108097;
RA   Yang W.P., Levesque P.C., Little W.A., Conder M.L., Shalaby F.Y.,
RA   Blanar M.A.;
RT   "KvLQT1, a voltage-gated potassium channel responsible for human
RT   cardiac arrhythmias.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:4017-4021(1997).
RN   [4]
RP   SEQUENCE OF 130-676 FROM N.A., AND VARIANTS LQT1.
RX   MEDLINE=96122034; PubMed=8528244;
RA   Wang Q., Curran M.E., Splawski I., Burn T.C., Millholland J.M.,
RA   Vanraay T.J., Shen J., Timothy K.W., Vincent G.M., de Jager T.,
RA   Schwartz P.J., Towbin J.A., Moss A.J., Atkinson D.L., Landes G.M.,
RA   Connors T.D., Keating M.T.;
RT   "Positional cloning of a novel potassium channel gene: KVLQT1
RT   mutations cause cardiac arrhythmias.";
RL   Nat. Genet. 12:17-23(1996).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM TKVLQT1).
RC   TISSUE=Heart;
RX   MEDLINE=97450920; PubMed=9305853;
RA   Jiang M., Tseng-Crank J., Tseng G.-N.;
RT   "Suppression of slow delayed rectifier current by a truncated isoform
RT   of KvLQT1 cloned from normal human heart.";
RL   J. Biol. Chem. 272:24109-24112(1997).
RN   [6]
RP   VARIANTS LQT1 SER-314 AND VAL-341.
RX   MEDLINE=97026293; PubMed=8872472;
RA   Russell M.W., Dick M. II, Collins F.S., Brody L.C.;
RT   "KVLQT1 mutations in three families with familial or sporadic long QT
RT   syndrome.";
RL   Hum. Mol. Genet. 5:1319-1324(1996).
RN   [7]
RP   VARIANTS LQT1 PRO-178; MET-313; ARG-325 AND PRO-366.
RX   MEDLINE=97176600; PubMed=9024139;
RA   Tanaka T., Nagai R., Tomoike H., Takata S., Yano K., Yabuta K.,
RA   Haneda N., Nakano O., Shibata A., Sawayama T., Kasai H., Yazaki Y.,
RA   Nakamura Y.;
RT   "Four novel KVLQT1 and four novel HERG mutations in familial long-QT
RT   syndrome.";
RL   Circulation 95:565-567(1997).
RN   [8]
RP   VARIANTS LQT1.
RX   MEDLINE=98045903; PubMed=9386136;
RA   Donger C., Denjoy I., Berthet M., Neyroud N., Cruaud C., Bennaceur M.,
RA   Chivoret G., Schwartz K., Coumel P., Guicheney P.;
RT   "KVLQT1 C-terminal missense mutation causes a forme fruste long-QT
RT   syndrome.";
RL   Circulation 96:2778-2781(1997).
RN   [9]
RP   VARIANT LQT1 ARG-216.
RX   MEDLINE=97418118; PubMed=9272155;
RA   van den Berg M.H., Wilde A.A.M., Robles de Medina E.O., Meyer H.,
RA   Geelen J.L.M.C., Jongbloed R.J.E., Wellens H.J., Geraedts J.P.M.;
RT   "The long QT syndrome: a novel missense mutation in the S6 region of
RT   the KVLQT1 gene.";
RL   Hum. Genet. 100:356-361(1997).
RN   [10]
RP   VARIANT LQT1 ASN-317.
RX   MEDLINE=98027069; PubMed=9302275;
RA   Wollnik B., Schroeder B.C., Kubisch C., Esperer H.D., Wieacker P.,
RA   Jentsch T.J.;
RT   "Pathophysiological mechanisms of dominant and recessive KVLQT1 K+
RT   channel mutations found in inherited cardiac arrhythmias.";
RL   Hum. Mol. Genet. 6:1943-1949(1997).
RN   [11]
RP   VARIANT LQT1 VAL-341.
RX   MEDLINE=98230121; PubMed=9570196;
RA   Li H., Chen Q., Moss A.J., Robinson J., Goytia V., Perry J.C.,
RA   Vincent G.M., Priori S.G., Lehmann M.H., Denfield S.W., Duff D.,
RA   Kaine S., Shimizu W., Schwartz P.J., Wang Q., Towbin J.A.;
RT   "New mutations in the KVLQT1 potassium channel that cause long-QT
RT   syndrome.";
RL   Circulation 97:1264-1269(1998).
RN   [12]
RP   VARIANT LQT1 THR-300.
RX   MEDLINE=98303396; PubMed=9641694;
RA   Priori S.G., Schwartz P.J., Napolitano C., Bianchi L., Dennis A.,
RA   de Fusco M., Brown A.M., Casari G.;
RT   "A recessive variant of the Romano-Ward Long-QT syndrome?";
RL   Circulation 97:2420-2425(1998).
RN   [13]
RP   VARIANT LQT1 SER-305.
RX   MEDLINE=98454341; PubMed=9781056;
RA   Neyroud N., Denjoy I., Donger C., Gary F., Villain E., Leenhardt A.,
RA   Benali K., Schwartz K., Coumel P., Guicheney P.;
RT   "Heterozygous mutation in the pore of potassium channel gene KvLQT1
RT   causes an apparently normal phenotype in long QT syndrome.";
RL   Eur. J. Hum. Genet. 6:129-133(1998).
RN   [14]
RP   VARIANTS LQT1 ARG-168; SER-314; CYS-315; ASN-318; PRO-353 & TRP-366.
RX   MEDLINE=98360095; PubMed=9693036;
RA   Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,
RA   Keating M.T.;
RT   "Genomic structure of three long QT syndrome genes: KVLQT1, HERG, and
RT   KCNE1.";
RL   Genomics 51:86-97(1998).
RN   [15]
RP   VARIANTS LQT1 ILE-312 AND ASN-317.
RX   MEDLINE=98141684; PubMed=9482580;
RA   Saarinen K., Swan H., Kainulainen K., Toivonen L., Viitasalo M.,
RA   Kontula K.;
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GenCore version 4.5


OM protein - protein search, using sw model

Run on: November 2, 2001, 12:02:04 ; Search time 27.64 Seconds
(without alignments)
465.994 Million cell updates/sec

Title: US-09-135-010A-113
Perfect score: 376
Sequence: 1 MNENAINSLYEAIPLPQDGS.....TWKIYIRKQSRNHHIMSPSP 376

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 4

Total number of hits satisfying chosen parameters: 60339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 71 | 18.9 | 604 | 1 | CIQ1_MOUSE | P97414 mus musculu |
| 2 | 69 | 18.4 | 676 | 1 | CIQ1_HUMAN | P51787 homo sapien |
| 3 | 20 | 5.3 | 695 | 1 | CIQ4_HUMAN | P56696 homo sapien |
| 4 | 13 | 3.5 | 872 | 1 | CIQ3_HUMAN | O43525 homo sapien |
| 5 | 10 | 2.7 | 528 | 1 | YJCC_ECOLI | P32701 escherichia |
| 6 | 7 | 1.9 | 119 | 1 | N4BM_HUMAN | O95298 homo sapien |
| 7 | 7 | 1.9 | 173 | 1 | CBX3_HUMAN | Q13185 homo sapien |
| 8 | 7 | 1.9 | 176 | 1 | VATL_ENTDI | Q24808 entamoeba d |
| 9 | 7 | 1.9 | 177 | 1 | VATL_ENTHI | Q24810 entamoeba h |
| 10 | 7 | 1.9 | 241 | 1 | YZ12_METJA | Q60274 methanococc |
| 11 | 7 | 1.9 | 244 | 1 | ATP6_BACSU | P37813 bacillus su |
| 12 | 7 | 1.9 | 256 | 1 | VBR1_CLVK | P03565 cassava lat |
| 13 | 7 | 1.9 | 261 | 1 | VBET_LAMBD | P03698 bacteriopha |
| 14 | 7 | 1.9 | 268 | 1 | PLSC_MYCGE | Q49402 mycoplasma |
| 15 | 7 | 1.9 | 332 | 1 | TBPA_HAEIN | P44984 haemophilus |
| 16 | 7 | 1.9 | 335 | 1 | TWK8_CAEEL | P34410 caenorhabdi |
| 17 | 7 | 1.9 | 387 | 1 | YHFX_ECOLI | P45550 escherichia |
| 18 | 7 | 1.9 | 395 | 1 | BIOI_BACSU | P53554 bacillus su |
| 19 | 7 | 1.9 | 460 | 1 | NU4M_ORNAN | Q36458 ornithorhyn |
| 20 | 7 | 1.9 | 474 | 1 | NU4M_PARTE | P15581 paramecium |
| 21 | 7 | 1.9 | 485 | 1 | VST2_HEVRH | Q00270 hepatitis e |
| 22 | 7 | 1.9 | 486 | 1 | MET2_YEAST | P08465 saccharomyc |
| 23 | 7 | 1.9 | 624 | 1 | SERA_ARATH | O04130 arabidopsis |
| 24 | 7 | 1.9 | 660 | 1 | VST2_HEVBU | P29326 hepatitis e |
| 25 | 7 | 1.9 | 660 | 1 | VST2_HEVMY | Q04611 hepatitis e |
| 26 | 7 | 1.9 | 660 | 1 | VST2_HEVPA | P33426 hepatitis e |
| 27 | 7 | 1.9 | 669 | 1 | FREL_CANAL | P78588 candida alb |
| 28 | 7 | 1.9 | 707 | 1 | DREB_RAT | Q07266 rattus norv |
| 29 | 7 | 1.9 | 722 | 1 | PALY_CITLI | Q42667 citrus limo |
| 30 | 7 | 1.9 | 752 | 1 | NEC1_RAT | P28840 rattus norv |
| 31 | 7 | 1.9 | 875 | 1 | POP1_YEAST | P41812 saccharomyc |
| 32 | 7 | 1.9 | 926 | 1 | CHS2_SCHPO | O74756 schizosacch |
| 33 | 7 | 1.9 | 1442 | 1 | CPSA_HUMAN | Q10570 homo sapien |
| 34 | 7 | 1.9 | 1444 | 1 | CPSA_BOVIN | Q10569 bos taurus |
| 35 | 7 | 1.9 | 1447 | 1 | SGS1_YEAST | P35187 saccharomyc |
| 36 | 6 | 1.6 | 52 | 1 | CRAB_TRASC | Q91518 trachemys s |
| 37 | 6 | 1.6 | 57 | 1 | V3A_IBVM | P05137 avian infec |
| 38 | 6 | 1.6 | 57 | 1 | V3A_IBVP3 | P30238 avian infec |
| 39 | 6 | 1.6 | 57 | 1 | V3A_IBVU5 | P30240 avian infec |
| 40 | 6 | 1.6 | 58 | 1 | V3A_IBVB | P30237 avian infec |
| 41 | 6 | 1.6 | 63 | 1 | ITHV_HIRMA | P81492 hirudinaria |
| 42 | 6 | 1.6 | 66 | 1 | CYT_SOLTU | Q03196 solanum tub |
| 43 | 6 | 1.6 | 66 | 1 | GVPA_AMOPE | P80998 amoebobacte |
| 44 | 6 | 1.6 | 71 | 1 | YVFE_VACCC | P20563 vaccinia vi |
| 45 | 6 | 1.6 | 72 | 1 | HTF_BLADI | Q17128 blaberus di |

ALIGNMENTS

RESULT 1
CIQ1_MOUSE
ID CIQ1_MOUSE STANDARD; PRT; 604 AA.
AC P97414;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 1 (KV1.9).
GN KCNQ1 OR KCNA9 OR KVLQT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97055937; PubMed=8900282;
RA Barhanin J., Lesage F., Guillemare E., Fink M., Lazdunski M.,
RA Romey G.;
RT "K(V)LQT1 and lsK (minK) proteins associate to form the I(Ks
RT potassium current.";
RL Nature 384:78-80(1996).
CC -!- FUNCTION: PROBABLY IMPORTANT IN CARDIAC REPOLARIZATION. ASSOCIATES
CC WITH KCNE1 (MINK) TO FORM THE I(KS) CARDIAC POTASSIUM CURRENT.
CC ELICITS A RAPIDLY ACTIVATING, K(+)-SELECTIVE OUTWARD CURRENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -!- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. KQT SUBFAMILY.
CC ---

CC ---
DR EMBL; U70068; AAB36518.1; -.
DR MGD; MGI:108083; Kcnq1.
DR InterPro; IPR000636; -.
DR Pfam; PF00520; ion_trans; 1.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT TRANSMEM 57 77 SEGMENT S1 (POTENTIAL).
FT TRANSMEM 83 103 SEGMENT S2 (POTENTIAL).
FT TRANSMEM 132 152 SEGMENT S3 (POTENTIAL).
FT TRANSMEM 197 217 SEGMENT S4 (POTENTIAL).
FT TRANSMEM 231 251 SEGMENT S5 (POTENTIAL).
FT TRANSMEM 263 283 SEGMENT S6 (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 604 AA; 68070 MW; 0E3579910F1CB697 CRC64;

Query Match 18.9%; Score 71; DB 1; Length 604;